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Result
No.
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
  222222221111111109
2654321098765432109
                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                  Match
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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US-08-438-123-16
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US-08-910-973-16
US-08-910-973-16
US-09-620-312D-653
US-09-367-750-1
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US-08-910-973-12
US-09-499-227-12
US-08-552-142A-10
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US-09-499-227-21
US-08-932-411A-17
US-09-419-568F-25
US-09-354-243B-25
US-09-453-702B-64
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US-09-499-227-10
US-09-234-332-3
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	Sequence 75, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 9532, Ap	Sequence 1904, Ap	Sequence 14810, A	Sequence 9635, Ap	Sequence 5, Appli	Sequence 5, Appli	Sequence 9622, Ap	Sequence 10, Appl	Sequence 8, Appli	Sequence 2, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli

ALIGNMENTS

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; NAME/KEY:
; LOCATION:
US-08-932-411A-19
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                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/932,411A FILING DATE: 15-SEP-1997 CLASSIFICATION: 536 PRIOR APPLICATION UNMBER: US 08/772,009 FILING DATE: 19-DEC-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                               TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Anderson,
APPLICANT: Ma, Qiufu
TITLE OF INVENTION: 1
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/
FILING DATE: 19-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,30
                                                           TOPOLOGY: unl
MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READMALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932,411A
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CORRESPONDENCE ADDRESS:
ADDRESSEE - TO RESE
                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEPAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Four Embarca
CITY: San Francisco
STATE: California
                                                                                                                  STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: United States ZIP: 94111-4187
                                                                                                                                       TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Flehr Hohbach Test Albritton & Herbert LLP Four Embarcadero Center, Suite 3400
                                                                                unknown
PE: DNA
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                   160..801
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RESULT 2
US-08-722-570-13
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                                                                                                          US-08-932-411A-13
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US-08-722-570-13
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Best Local Similarity 100.0%;
Matches 92; Conservative
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Patent No. 6
                                                                         Patent No.
                                                                                       Sequence 13, Application US/08932411A
                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                               Query Match 1.6%; Score 23; Best Local Similarity 100.0%; Pred. No.
               GENERAL INFORMATION:
APPLICANT: Anderson, David J.
APPLICANT: Ma, Qiufu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-63
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Anderson, David J. APPLICANT: Ma, Qiufu TITLE OF INVENTION: NEUROGENIN NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 738 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/722,570 FILING DATE: 27-SEP-1996 CLASSIFICATION: 5365
                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
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                                                                                                                                                                                        304 GAGCGCAACCGCATGCACAACCT 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRY: United States 94111-4187
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California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (415) 398-3249
                                                                                                                                                                                                                                                               Conservative
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NEUROGENIN
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Pred. No.
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US-08-910-973-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 base
                                                                                                                                                                                                                                                                                                     Patent No. 5795723
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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FILING DATE: 15-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/772,009
FILING DATE: 19-DEC-1996
PRIOR APPLICATION NUMBER: US 08/722,570
FILING DATE: 19-DEC-1996
ATTORNEY/AGENT IMPORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 3,304
REFERENCE/DOCKET NUMBER: A-63902-3/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                Sequence 21,
                                                                                                                                                                                                    APPLICANT: Tapscott, Stephes
APPLICANT: Olson, James M.
TITLE OF INVENTION: Express
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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          ZIP: 98.01-2347
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 781-198
TELEPAX: (415) 398-3249
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                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
                                                                                                                                                                        ADDRESSEE: Christensen O'Connor Johnson KindnessPLLC
STREET: 1420 Fifth Avenue, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                               304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   732 GAGCGCAACCGCATGCACAACCT 754
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94111-4187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                     Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGCGCAACCGCATGCACAACCT 326
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                                                                                                                                   WA
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                                                                                                                                                                                                                                                                                                                                                Application US/08910973
                                                                                                                 USA
                                                                                                                                                                                                                                                                                       Tapscott, Stephen J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
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100.0%; Pred. No. 0.
ative 0; Mismatches
                                                                                                                                                                                                                                                  Expression of Neurogenic bHLH Genes in Primitive Neuroectode:
Release #1.0,
  Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 738;
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-Q=/cgn2 1/USPTO spool/US09595947/runat 02022004 154933 8046/app query.fasta_1.391
-DB=GenEmb1 - CPMT=fastap -SUFFLX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-LUNITS=blts -START=1 -END=-1 -MATRIX=blosum62 -TRANS=buman40.cd1 -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=axt -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0959547 @GCN 1 _3508 @runat _02022004 154933 8046 -NCPU=6 -ICPU=3
-NO MMAP -LARGGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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-MODEL=frame+_p2n.model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Ravassard, P.
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AJ133776.1 GI:5123782
bHLH transcription fact
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SPGGPPGDWGSLYSPVSQAGSLSPAASLEERPGHLGARSSACLSPGSLAFSDFL"
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/mol_type="genomic DNA"
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Mutations in the coding region of the neurogenin 3 gene (NEUROG3)
are not a common cause of maturity-onset diabetes of the young in
Japanese subjects
Diabetes 50 (3), 694-696 (2001)
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del Bosque-Plata, L., Lin, J., Horikawa, Y., Schwarz, P.E., Cox, N. J.,
Iwasaki, N., Ogata, M., Iwamoto, Y., German, M.S. and Bell, G.I.
                                                                                                                                                                                                                   Submitted (15-FBB-2000) Hormone Research Institute, University of California San Francisco; 513 Parnassus Ave., San Francisco, CA
                                                                                                                                                                                                                                                    2 (bases 1 to 5340)
Lin, J. and German, M.
Direct Submission
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  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                         Homo sapiens
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MCAEAEEGGCRGAPRKLFARRGGRSRPKSELALSKQRESERKANDREEMRMHNLNSA
LDALRGVLPTFPDDAKLTKLETLRFAHNYIMALTQTLRIADHSLYALEPPAPHCGELG
SPGGSPGDWGSLYSPVSQAGSLSPASILEERPGLLGATSSACLSPGSLAFSDFL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               left end of clone RP11-242G20 is at 139955 in this sequence. The true right end of clone RP11-404C6 is at 6588 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VECTOR: pBACe3.6
This sequence is the entire insert of clone RP11-343J3 The true
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences we only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.sanger.ac.uk/HGP/Chr10
RP11-343J3 is from the library RPCI-11.2 constructed of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               During sequence assembly data is compared from overlapping clones Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          requests: clonerequest@sanger.ac.uk
On Jul 8, 2001 this sequence version replaced gi:14575291.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="10"
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                                                                                                                                                                                                                                                                                                        note="L1MEc repeat:
                                                                                                                                                                                                                                                                                                                                                                                   note="AluSx repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="26 copies 2 mer gt 98% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="MIR repeat: matches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="THE1C repeat: matches 2. .142 of consensus"
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                                                                                                                           .11639
                                         .13876
                                                              mer at 90% conserved"
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                                                                                                                                                                                                                                                                                                                                                                                                                               matches 1. .310 of consensus"
                                                                                                                                                                                                                                                                                                          matches 272. .1095 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                     matches 1.
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                                                                                                                                                                                   .194 of consensus"
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                                                                                                                                             .294 of consensus"
                         .466 of consensus"
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/note="CpG island"
/evidence=not experimental
36551..36604
/note="27 copies 2 mer ac:
37585..38254
                                                                                                                                                                                                                                                                                       /evidence=not_experimental
29453. .30918
/note="CpG island"
                                                                                                                                                                                                                                                                                                                                                                                                                       24291. .24581
note="AluSx repeat: matches 1. .300 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MIR repeat: matches 48. .188 of consensus"
23388. .23532
| note="12 repeat: matches 2097. .2230 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MLT1J repeat: matches 117. .413 of consensus"
23215. .23346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MLT1F repeat: matches 188. .541 of consensus"
21463. .21618
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note="21 cop
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.note="LIMC5 repeat: matches 7728. .7917 of consensus"

19642. .19716

.note="MIR repeat: matches 48. .131 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="12 repeat: matches 1754. .2097 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="AluJb repeat: matches 1.
23838. .24137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="L2 repeat: matches 2453. .2629 of consensus"
!2896. .23174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="MIR repeat: matches 46. .192 of consensus"
22019. .22326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="MLT1J repeat: matches 1. .62 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="U2 repeat: matches 1. .36 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="41 copies 2 mer gt 85% conserved"
10738. .20773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="MBR86 repeat: matches 9. 5404. .15613
                                                                                              note="43 copies 3
35112. .36201
                                                                                                                                                                         note="AluJo repeat: matches 29.
12767. .32830
                                                                                                                                                                                                                                                      evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="33 copies 2 7476. .17569
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                                                                                                                                                     note="MIR repeat: matches 76.
                                                                                                                                                                                                                                note="MIR repeat: matches 65. .138 of consensus"
                                                                                                                                                                                                                                                                                                                                                                  note="MIR repeat:
6189. .26685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="AluJb repeat: matches 1. .306 of consensus"
2381. .22564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0623. .20704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="MER81 repeat: matches 2. .114 of consensus'
7719. .18069
                                                                                                                                                                                                                                                                                                                                                note="CpG island"
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                                                                                                                                                                                                                . .31876
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                   mer ac 94%
                                                                                                                mer tcc
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38265. .38561
/note="Alusx repeat: matches 1. .300 of consensus"
                                                                                                                                                                                                                                                                                                            52222...52519
/note="AluSx repeat: matches 1. .300 of consensus"
54065...54260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MIR repeat: matches 3. .219 of consensus"
19489. .39801
/note="AluSx repeat: matches 1. .292 of consensus"
10050. .40189
/note="MIR repeat: matches 1. .144 of consensus"
1057. .41290
                                                                                                                                                                                                       /note="L1M4 r
54648. .54862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14600. .44956 inote="ITR16A repeat: matches 90. .445 of consensus" 15240. .45300 inote="MER58A repeat: matches 37. .97 of consensus" 15798. .45909
                                                                                                                                                                                                                                        4433. .54629
                                                                                                                                                                                                                                                                            note="L1M4 repeat: matches 3865. .4055 of consensus" 4261. .54432
                                                                                                                                                                                                                                                                                                                                                                                                     note="Alusq repeat: matches 1. .287 of consensus"
                                                                                                                                                                                  note="LTR41 repeat: matches 11.
                                                                                                                                                                                                                                                           note="FAM repeat: matches 2. .167 of consensus"
                                                                                                                                                                                                                                                                                                                                                                   0980. .51291
note="AluSx repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="L2 repeat: matches 1448. .1779 of 4193. .44579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2388. .42698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="L2 repeat: matches 2569. .2730 of consensus"
1506. .41944
1.42e-43
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98.13%
97.52%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e="LTR41 repeat: matches 90.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e="L2 repeat: matches 1916. .2416 of consensus"
                                                                                                                                                                                                                      repeat: matches 3652.
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                                                       Length:
Matches:
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Birren, B., Linton, L., Nusbaum, C., Lander, B., Abraham, H., Allen, N. Anderson, S., Baldwin, J., Barna, N., Bastlen, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grant, G., Hagos, B., Heaford, A., Horton, L., Grant, G., Johnson, R., Jones, C., Kann, L., Karatas, A.
                                                                                                                                                                                                                                                                                            Submitted (22-JAN-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 173341)
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1 (bases 1 to 173341)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens chromosome 10, clone RP11-57E12
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HTG; HTGS_PHASE1; HTGS_DRAFT
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submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 5, 2000 this sequence version replaced gi:6984451.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Insert size: 176000; agarose-fp
Insert size: 171041; sum-of-contigs
Quality coverage: 3.7 in Q20 bases;
Quality coverage: 3.8 in Q20 bases;
                                                                                                                                                                Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 161190 bases at least Q40 Consensus quality: 166837 bases at least Q30 Consensus quality: 166837 bases at least Q20 Consensus quality: 168995 bases at least Q20
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Center clone name: 57_E_12
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COMMENT JOURNAL

as soon as it is available and the accession number will be preserved. 27487 32573 32673 32673 38633 38733 43736 43736 43836 49021 49021 18832 18932 23527 23627 27387 1575 1675 3044 3144 3144 5890 5990 8980 9080 13675 13775 43835 1574: 1674: contig gap of gap of contig gap of contig gap of contig gap of contig gap o contig gap of g of 2746 bp f 100 bp f 100 bp f 106 2990 bp f 106 299 bp g of 4595 bp f 100 bp g of 5057 bp f 100 bp 100 bp of 5003 100 bp of 5185 100 bp 100 bp of 4595 100 bp of 3760 100 bp of 4540 100 bp of 1574 bp in length 100 bp of 1369 bp in length 100 bp å ģ ďq g ď in length in length in Ħ in ij ä 'n in length ij in length length length length length length length length

runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown

consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record is

NOTE: This is a 'working draft' sequence. It currently

consists of 24 contigs.

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59644: gap of 100 bp
66395: contig of 6751 bp in length
66495: gap of 100 bp
74696: contig of 8201 bp in length
74796: gap of 100 bp
81326: contig of 6530 bp in length
81426: gap of 100 bp
89446: contig of 8020 bp in length
89546: gap of 100 bp
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117086: gap of 100 bp
128890: contig of 11804 bp in length
128990: gap of 100 bp
147390: gap of 100 bp
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128991_ .147290
/note="assembly_fragment"
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Muridae;

Euteleostomi; Murinae;

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GGTAGCCTGAGCCCCACAGCCTCATTGGAGGAGTTCCCTGGCCTGCAGGTGCCCAGCTCC
                                                                                    (bases 1 to 1491)
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/db_xref="G1:6740203"
/db_xref="G1:6740203"
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/mol_type="genomic DNA"
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459. .1103
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PD 31-UUL-2001

PF 19-DEC-1997 JP 1998527415

PR 19-DEC-1996 FR 96/15551

PI CHRISTINE ICARD LIEPKALNS, JACQUES MALLET, PHILIPPE RAVASSARD PC C07K14/47, A61K31/711, A61K35/76, A61K38/00, A61K48/00, A61P25/00, PC C12N15/09, PC C12N15/09, CC Strandedness: Single;

CC Topology: Linear.

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Liepkalns, C.I., Mallet, J. and Ravassard, P.
Polypeptide belonging to the family of basic helix-loc
(bHLH) family and nucleic acid sequence corresponding
Patent: JP 2001510464-A 1 31-JUL-2001;
RHONE POULENC RORER A
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Relax, a novel rat bHLH transcriptional regexpressed in the ventricular proliferating
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                      Paris,
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de la Pitie Salpetriere,
                                              /protein id="CAA71630.1"
/db_xref="G1:2072738"
/db_xref="G1:2072738"
/db_xref="G1:2072738"
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LDALRGVLPTFPDDAKLTKLETLRAHNYIWALTQTLRIADHSFYGPEPPVFCGELGS
PGGGSSGDWGSIYSPVGQAGSLSPTASLEEFPGLQVPSSPSCLLPGTLVFSDPL"
a 487 c 413 g 284 t
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                                                                                                                                                                                          codon_start=1
                                                                                                                                                                                                         function="transcriptional regulator"
                                                                                                                                                                                                                                         'clone
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                                                                                                                                                                                                                                                                        strain="Wistar"
                                                                                                                                                                                                                                                                                                      organism="Rattus norvegicus"
                                                                                                                                                                                                                                         _xref="taxon:10116"
one_lib="RT-pCR"
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; Murinae;
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Best Local Similarity:
                                                                                               REFERENCE
                                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                                                       DEFINITION
                                                                                AUTHORS
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1 (bases 1 to 258815)
Muzny, D. Marie., Metzker; M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranalke, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blainkenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
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                                                                                                                        AC127817.3 GI:25077905
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                         Rattus norvegicus clone
                                                                                                              Rattus.
                                                                                                                                                                                                                                       unordered pieces.
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878 140 818 120 758 100 869 80 638 60

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HTG 19-NOV SEQUENCE,

19-NOV-2002

Euteleostomi; Murinae;

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Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox., Coyle, M., Cree, A., D'Souza, I., Davis, C., Davy, Carroll, L., De, Anda C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Daylla, M.L., Davis, C., Davy, Carroll, L., De, Anda C., Dederich, D., Delgado, O., Denson, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagy, M., Forbes, I., Foster, M., Garrar, M., Gabisi, A., Ganta, R., Garcia, A., Garrar, M., Gavara, W., Ghisi, A., Ganta, R., Garcia, A., Garrar, M., Gavara, W., Gunarathe, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harrandez, J., Harray, Y., Havlak, S., Hladdın, S.I., Hodgson, A., Hogues, M., Hernandez, J., Handez, R., Hines, S., Hladdın, S.I., Hodgson, A., Hogues, M., Hernandez, J., Harray, Y., Havlak, S., Hune, J., Idhshird, D., Jackson, A., Jackson, A., Hollins, B., Howella, S., Hulyk, S., Hune, J., Idhshird, D., Jackson, A., Jackson, A., Hollins, B., Howella, S., Hulyk, S., Hune, J., Idhshird, D., Jackson, A., Jackson, A., Honger, J., Liu, Y., London, P., Longere, S., Lopez, J., Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Liu, Y., London, P., Longere, S., Lopez, J., Loussey, M., Martin, R., Martinez, E., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhinley, S., McLeod, M.P., McNeill, T. Z., Meenen, E., Mayna, M., Norris, S., Munidasa, M., Marphy, M., Naix, L., Mayna, M., Norris, S., Munidasa, M., Marphy, M., Naix, L., Nankervis, C., Nedlay, T., Royla, R., Reigh, R., Reily, B., Reily, M., Steon, J., Stever, S., Scott, G., Shateman, S., Shen, H., Shen, H., Walker, B., Wang, J., Warren, R., Welke, R., Walker, B., Wang, J., Walker, 
                                                                           Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:23912578.
On Nov 19, 2002 this sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 258815)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat Genome Sequencing Consortium.
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----- Genome Center
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REFERENCE AUTHORS TITLE JOURNAL

REFERENCE AUTHORS TITLE

JOURNAL

TITLE JOURNAL

COMMENT

Center: Baylor College

of Medicine

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US-09-595-947E-10 (1-214) x AC127817 (1-258815)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similari
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                                                  247980 CTCGTACCGAGGGACTGCTCCGAAGCAGAAGCAGGTGACTGCCGAGGGACATCGAGGAAG 248039
                                                                                                                                                       247920
                                                                                                                                                                                                                                                      247860 ATGGCGCCTATCCCTTGGATGCGCCCACCATCCAAGTGTCCCAAGAGAGACCCAGCAACCC 247919
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity:
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61 LeuArgAlaArgArgGlyGlyArgSerArgProLysSerGluLeuAlaLeuSerLysGln 80
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

(NOTE: This is a "working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                   MetThrProGlnProSerGlyAlaProThrValGlnValThrArgGluThrGluArgSer
                                                                                                                                                       TTTCCCGGAGCCTCGGACCACGAAGTGCTCAGTTCCAATTCCACCCCACCTAGCCCCACT 247979
                                                                                                                                                                                                 PheProArgAlaSerGluAspGluValThrCysProThrSerAlaProProSerProThr 40
                                                                                                  ArgThrProGlyAsnCysAlaGluAlaGluGluGlyGlyCysArgGlyAlaProArgLys 60
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Center clone name: CH220-259G16

Center clone name: CH2210-259G16

Center Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 224747 bases at least Q40

Consensus quality: 227981 bases at least Q30

Consensus quality: 229792 bases at least Q20

Estimated insert size: 228243; sum-of-contigs estimation Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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clone_end:Sp6"
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56888 c 58131 g 56
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clone_end:T7
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/db_xref="taxon:10116"
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256079: gap of unknown length
257349: contig of 1270 bp in length
257349: gap of unknown length
257449: gap of 1366 bp in length.
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DeveloGen Aktiengesellschaft fuer Entwicklungsbiologische Forschung
(DE); INSTITUT FUER PFLANZENGENETIK UND KULTURPFLANZENFORSCHUNG
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/db_xref="G1:29499590"
/db_xref="G1:29499590"
/translation="MAPHPLDALTIQVSPETQQPFPGASDHEVLSSNSTPPSPTLIPR
DCSEAEVGDCRG7SRKLRARRGGRNRPKSELALSKQRRSRKKANDRERNRMHNINSA
LDALRGVLPTFPDDAKLTKIETLRFAHNYIWALTQTLRIADHSFYGPEPPVPCGELGS
                                                                                                                                                              PGGGSNGDWGSIYSPVSQAGNLSPTASLEEFPGLQVPSSPSYLLPGALVFSDFL"
                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
|mol_type="genomic DNA"
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                     Sommer, L., Ma,Q. and Anderson,D.J.

Direct Submission
Submitted (24-OCT-1996) Biology 216-76, California Institute of Technology, Howard Hughes Medical Institute, Pasadena, CA 91125, USA
                                                                                                                                           neurogenins, a novel family of atomal-related bHLH transcription factors, are putative mammalian neuronal determination genes that reveal progenitor cell heterogeneity in the developing CNS and PN mol. Cell. Neurosci. 8 (4), 221-241 (1996)
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Schwitzgebel, V. and German,
Direct Submission
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Sciurognathi; Muridae;
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                                                                   Direct Submission
Submitted (01-AUG-2000) Lemaigre F.P., Hormone and Metabolic Submitted (01-AUG-2000) Lemaigre F.P., Hormone and Metabolic Research Unit, Louvain University Medical School, Avenue Hipp 75, box 7529, Brussels 1200, BELGIUM On Oct 31, 2000 this seguence version replaced gi:1666087.
                                                                                                                                                                                                       Direct Submission
Submitted (04-NOV-1996) G.J. Gradwohl,
CNRS-INSERM-Universite Louis Pasteur, |
F-67404 ILLKIRCH cedex, FRANCE
                                                                                                                                                                                                                                                                                                                         Mol. Cel:
20285449
                                                                                                                                                                                                                                                                                                                                   Transcription factor hepatocyte nuclear factor 6 regulates pancreatic endocrine cell differentiation and controls export the proendocrine gene ngn3 cell. Biol. 20 (12), 4445-4454 (2000)
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Y09167
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Mammalia; Eutheria; Rodentia;
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="SV129"
                                                           Location/Qualifiers
                                               .5567
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Sciurognathi; Muridae;
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SerPro---GlyGlyProProGlyAspTrpGlySerLeuTyrSerProValSerGlnAla 179
                                                               IleAlaAspHisSerLeuTyrAlaLeuGluProProAlaProHisCysGlyGluLeuGly
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                                  ATAGCGGACCACAGCTTCTATGGCCCGGAGCCCCCTGTGCCC--
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/cell_type="embryonic stem cells"
/clone lib="Genomic library No.62,
cloned in BamHI"
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/db_xref="$WISS_POOT: P70661"
/db_xref="$WISS_POOT: P70661"
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DCSEAEVGDCGTSKLRARRGGRNRPKSELALSKQRRSRRKKANDRERNRMHNLNSA
DDALRGVLPTFDDAKLTKLETLRFAHNYIWALTQTLRIADHSFYGDEPPVPCCELGS
PGGGSNGDWGSIYSPVSQAGNLSPTASLEEFPGLQVPSSPSYLLPGALVFSDFL"
1549 c 1564 g 1183 t.
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4145. .4151
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/protein_id="CAA70366.1"
/db_xref="GI:1666088"
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4145. .5567
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/clone="lambda GEM12 clone
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/codon_start=1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 138070)

McCombie, W.R., Baker, J.P., Balija, V., Dedhia, N.N., de la Bastide, M., Katzenberger, F., Kuit, K., King, L., Kirchoff, K.A., Miller, B., Muller, S., Nascimento, L.U., O'Shaughnessy, A.L., Preston, R.R., Santos, L., Spiegel, L.A., Palmer, L., Yang, C. and
                                                                                                                                                                                                                                                                                                                                                                                  Insert size: 173000; agarose-fp
Insert size: 141616; sum-of-contigs
Quality coverage: 4.00 in Q20 bases; agarose-fp
Quality coverage: 3.70 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.cshl.org/genseq Contact: mccombie@cshl.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Lita Annenberg Hazen Genome Center, Cold
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Harbor, NY 11724, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (07-FEB-2002) Lita Annenberg Center, Cold Spring Harbor Laboratory,
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Mus musculus clone RP23-121F10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone name: RP23-121F10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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6: contig of 12482 bp in length
4: gap of unknown length
6: contig of 11862 bp in length
6: contig of 11862 bp in length
8: contig of 11804 bp in length
6: gap of unknown length
5: contig of 10669 bp in length
5: contig of 9573 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus chromosome UNK clone RP23-459M2, WORKING SEQUENCE, 7 unordered pieces.
AC127417
AC127417.2 GI:24137619
HTG; HTGS PHASE1; HTGS DAFT; HTGS FULLTOP.
Mus musculus (house mouse)
Mus musculus (house mouse)
Mus musculus
Eukarvara.
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: plasmid; 100% Chemistry: Dye-primer ET; 0% of reads Chemistry: Dye-terminator Big Dye; 100% of re Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.990319 Consensus quality: 212279 bases at least Q40 Consensus quality: 213137 bases at least Q30 Consensus quality: 213590 bases at least Q20 Consensus quality: 213590 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Washington University Genome Sequencing Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (19-OCT-2002) Genome Sequencing Center, 4444 Forest Parkway, St. Louis, MO 63108, USA
On Oct 19, 2002 this sequence version replaced gi:21759524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (15-JUL-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (Dases 1 to 215050)
McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 215050)
McPherson, J.D. and Waterston, R.H.
Direct Submission
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McPherson, J.D. and Waterston, R.H.
The sequence of Mus musculus clone
                                                                                                                                                                                                                                                                                                                                      Insert size: 192000; agarose-fp
Insert size: 217944; sum-of-contigs
Quality coverage: 11.89 in Q20 bases; agarose-fp
Quality coverage: 10.54 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site:http://genome.wustl.edu/gsc/index.shtml Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: M13;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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                                                                                                                                       as soon as it is available and the accession number will be preserved.
      4228
4328
16590
16690
27319
4227: contig of 4227 bp in length
4327: gap of unknown length
16589: contig of 12262 bp in length
16689: gap of unknown length
27318: contig of 10629 bp in length
27418: gap of unknown length
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Percent Similarity:
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Query Match:
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ATAGCGGACCACAGCTTCTATGGCCCGGAGCCCCCTGTGCCC--
                      IleAlaAspHisSerLeuTyrAlaLeuGluProProAlaProHisCysGlyGluLeuGly
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132696. .215050
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27419. .49797
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="UNK"
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49898. .79378
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52513 c 52885 g 53012 t
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49897: gap of unknown length
79378: contig of 29481 bp in length
79478: gap of unknown length
132595: contig of 53117 bp in length
132695: gap of unknown length
132695: gap of unknown length
135050: contig of 82355 bp in length
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AUTHORS
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* NOTE: This is a 'working draft' sequence.
* consists of 21 contigs. The true order of
* is not known and their order in this seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (29-SEP-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 28, 2000 this sequence version replaced gi:6479051. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Homo sapiens clone RP11-6P16, WORKING DRAFT SEQUENCE,
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Homo sapiens, clone RP11-6P16
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                      Sequencing vector: M13, M77815; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 114103 bases at least Q40 Consensus quality: 14155 bases at least Q30 Consensus quality: 158230 bases at least Q20 Insert size: 154000; agarose-fp Insert size: 168896; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                        Center project name: L2916 Center clone name: 6_P_16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                          Quality coverage: 3.6 in Q20 bases; agarose-fp Quality coverage: 3.3 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WIBR
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
ocation/Qualifiers
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                                                                     Leu 214
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Search completed: February Job time: 3780 secs

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6, -DELEXT=7
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Listing first 45 summaries
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution

SUMMARIES

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Key Location/Qualifiers CDS 30223666	Homo sapiens.		islet cell precursor identification; diabetes mellitus; human; ds.	Neurogenin 3; Ngn3; chromosome 10q22.1-22.2; cellular differentiation;		Human neurogenin 3 (Ngn3) genomic DNA sequence.		05-FEB-2001 (first entry)		AAC61089;		AAC61089 standard; DNA; 5340 BP.	1089	LT 1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein AAY85617. The Ngn3 gene is located at chromosome position 10q22.1-22.2. The invention relates to the human Ngn3 nucleotide and protein sequences, and includes an antibody recognising the Ngn3 protein. Also included in the invention is a method for identifying an islet cell precursor, the method involves analysing a cell for the expression of the Ngn3 gene product, where detection of the product is indicative of an islet cell precursor. The Ngn3 DNA sequence is useful as a diagnostic reagent for detecting (in a subject) a predisposition to a defect in pancreatic islet cell function or formation associated with a defect in Ngn3 activity. The Ngn3 protein is useful for identifying beta-cell precursor cells expressing Ngn3, and to alter cellular differentiation in culture in vivo to produce new beta-cells to treat patients with diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The human neurogenin 3 Ngn3 DNA sequence AAC61089 encodes the Ngn3 protein AAY85617. The Ngn3 gene is located at chromosome position
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human neurogenin 3 polypeptides and polynucleotides encoding them, useful for diagnosis, prevention and treatment of diabetes mellitus and to identify individuals at risk of diabetes -
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                                                                                                                                                                                                                                                 Producing a mammalian islet cell for treating diabetes mellitus comprises introducing into a mammalian cell a nucleic acid molecule encoding neuroendocrine basic helix-loop-helix transcription factor
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The invention relates to a method for producing a mammalian islet cell. The method comprising introducing into a mammalian cell a nucleic acid molecule encoding an islet transcription factor for expression of the islet transcription factor in the cell and for production of islet cell phenotype in the cell. The islet transcription factor is a neuroendocrine basic helix-loop-helix (bHLH) transcription factor. The method is useful for treating type 2 diabetes mellitus and for replacing beta cells lost

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to autoimmune destruction in individuals with type 1 diabetes. The method is useful in cell therapy. The present sequence is human neurogenin 3 (Ngn3) gene. Ngn3 gene is located on chromosome 10q22.1-22.2.
control; gene expression; protein expression; centra
                                                        05-OCT-1998
                                                                                            AAV42512 standard;
        Basic helix-loop-helix; BHLH; RELAX; Rat Embryonic Longitudinal control; gene expression; transcriptional activator; targeting;
                                                                         AAV42512
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                                                                                                                                                                                     SerLeuSerProAlaAlaSerLeuGluGluArgProGlyLeuLeuGlyAlaThrSerSer
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                                                                                                                                                                                                                                                                                 AAGATCGAGACGCTGCGCTTCGCCCACAACTACATCTGGGCGCTGACTCAAACGCTGCGC
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                                    protein designated RELAX.
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes a basic helix-loop-helix (BHLH) type protein, designated RELAX (Rat Embryonic Longitudinal Axis) protein. The protein is used to control and participate in gene expression, by acting as transcriptional activator, strictly dependent on the presence of an intact E box (CANNTG), particularly for targeting expression of proteins to the central nervous system (CNS). The nucleic acid sequence can be used to treat nervous system disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Basic helix-loop-helix polypeptide and related nucleic transcriptional activity, for targeting expression of greentral nervous system and treatment of nervous disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Page 20; 28pp; French.
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SerAlaLeuAspAlaLeuArgGlyValLeuProThrPheProAspAspAlaLysLeuThr
                                                                                      ArgArgSerArgArgLysLysAlaAsnAspArgGluArgAsnArgMetHisAspLeuAsn
                                                                                                                                                                LeuArgAlaArgArgGlyGlyArgSerArgProLysSerGluLeuAlaLeuSerLysGln
                                                                                                                                                                                                                       CTCGTACCGAGGGACTGCTCCGAAGCAGAAGCAGGTGACTGCCGAGGACATCGAGGAAG
                                                                                                                                                                                                                                                                                                                                                                               ATGGCGCCTCATCCCTTGGATGCGCCCACCATCCAAGTGTCCCAAGAGACCCAGCAACCC
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                                                               CGACGAAGCCGGCGCAAGAAGGCCAACGACCGGGAGCGCAACCGCATGCACAACCTTAAC
                                                                                                                                           ArgThrProGlyAsnCysAlaGluAlaGluGluGlyGlyCysArgGlyAlaProArgLys
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          The Mouse neurogening. The neurogening in the present invention. The neurogening in a host cell, transformed using an expression vector, recombinant proteins. The proteins and the antibodies is a contract of the study of neurogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                             17-SEP-1997;
27-SEP-1996;
12-NOV-1996;
19-DEC-1996;
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acids
    Sequence
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                                                                                                neurogenin 3 is one of several neurogenin proteins discussed esent invention. The neurogenin nucleic acids can be expressed
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Best Local Similarity:
                                   Neurogenin-3; NGN-3; non-neuronal cell; NNC; neurogenesis; PhoxZa protein; neuronal subtype-specific marker; growth factor neural differentiation; transplanen; neuronal dysfunction; optical nerve damage; auditory nerve damage, neurodegenerative neuroprotective; nootropic; anticonvulsant; antiParkinsonian; v cerebroprotective; immunesuppressant; antiinfectious; ds.
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                                                                                                                                   neurogenin-3 (NGN3) nucleic acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The patent discloses a method for inducing non-neuronal cells (NNC) to differentiate into neurons and for NNCs to express a neuronal subtype specific marker. Transformed host cells are used as sources of neuronal and other growth factors; in culture for screening compounds that modulate neural differentiation or as sources of recombinantly produced neurogenins and phox2a proteins for use in transplantation. The cells also have a variety of in vivo uses, e.g. for transplantation at sites of neuronal dysfunction e.g. patients with hearing or vision loss due to optical or auditory nerve damage, brain or spinal cord injuries, and neurodegenerative discaders e.g. Alzheimer's disease. The present sequence encodes murine neurogenin-3 (NGN-3), a transcription factor. NNCs differentiate into neurons through the recombinant expression of a transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transcription factor that induces a core program of neurogenesis. expression of murine NGN3 can elicit expression of at least some r phenotypic markers even in NNCs.
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The invention relates to the use of atonal-associated nucleic acid amino acid sequence, or any of its homologues or orthologues as therapeutic agents for the treatment of deafness, partial hearing lyestibular effects due to damage or loss of inner hair cells, osteoarthritis and abnormal cell proliferation. The invention also encompasses methods of screening for compounds which affect the expression of an atonal-associated nucleic acid sequence in an anim
                                                                                                                                          Therapeutic use of atonal-associated nucleic acids or amino acids, or any of its homologs or orthologs, for the treatment of e.g. deafness, osteoarthritis and abnormal cell proliferation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Atonal; homologue; orthologue; atonal-associated protein; deafness; hearing impairment; vestibular effect; balance disorder; osteoarthritis; cellular proliferation; cerebellar granule neuron; gene therapy; mechanoreceptive cell growth; auditory; osteopathic; cytostatic;
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                                                                                                               Disclosure; Page -; 142pp; English.
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Note: The present sequence is not shown in the specification, but
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ABV75970 ID ABV7

ABV75970 standard; cDNA; 861 BP

Percent Similarity:
Best Local Similarity:
Query Match:

1.45e-42 819.00 82.33% 75.81% 72.67%

Length:
Matches:
Conservative:
Mismatches:

861 163 14 36 2

Indels:

Score:

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The present sequence is that of cDNA encoding the murine CC basic helix-loop-helix transcription factor neurogenin 3 (ngn3), CC a gene which is required for the specification of the early CC endocrine precursor in the pancreatic epithelium and which is CC down-regulated once endocrine differentiation begins. The invention CC provides a claimed method for differentiation stem cells (especially cembryonic, adult or somatic stem cells and primordial germ cells) into insulin-producing cells. This involves culturing stem cells in CC a suitable medium and activating at least one gene involved in CC beta-cell differentiation. Preferred genes including Pdx1, Pax4, CC Pax6 and ngn3 (see ABV75967-70). Gene activation comprises the CC delivery of the gene into stem cells can be transplanted into cells. The insulin-producing cells can be transplanted into CC syndrome and metabolic disorders with impaired glucose levels such CC as diabetes, hyperglycaemia and impaired glucose tolerance (claimed). The cells can also be used to identify compounds which CC into the case of idifferentiated beta-cells can be used to beta-cell cifferentiated beta-cells can be used to study the toxic and other effects of exogenous compounds on beta-cell cinto expression vector pACCMV.pLpA under the control of the cytomegalovirus promoter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Differentiating stem cells into insulin-producing cells useful for treating pancreatic diseases, by culturing stem cells in suitable medium and activating gene involved in beta-cell differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 58-59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method for producing a mammalian islet cell. The method comprising introducing into a mammalian cell a nucleic acid molecule encoding an islet transcription factor for expression of the islet transcription factor in the cell and for production of islet cell phenotype in the cell. The islet transcription factor is a neuroendocrine basic helix-loop-helix (bHLH) transcription factor. The method is useful for treating type 2 diabetes mellitus and for replacing beta cells lost to autoimmune destruction in individuals with type 1 diabetes. The method is useful in cell therapy. The present sequence is murine neurogenin 3 manual form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Producing a mammalian islet cell for treating diabetes mellitus comprises introducing into a mammalian cell a nucleic acid molecule encoding neuroendocrine basic helix-loop-helix transcription factor
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P-PSDB; AAE29278.
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SerPro---GlyGlyProProGlyAspTrpGlySerLeuTyrSerProValSerGlnAla 179
                                                  IleAlaAspHisSerLeuTyrAlaLeuGluProProAlaProHisCysGlyGluLeuGly
                                                                                         AAGATICGAGACCCTGCGCCTTCGCCCACAACTACATCTGGGCACTGACTCAGACGCTGCGC
                                                                                                        LysIleGluThrLeuArgPheAlaHisAsnTyrIleTrpAlaLeuThrGlnThrLeuArg
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                             ATAGCGGACCACAGCTTCTATGGCCCGGAGCCCCCTGTGCCC---TGTGGAGAGCTGGGG
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Alignment Scores: Pred. No.:
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                                                                               protein sequences, and includes an antibody recognising the Ngn3 protein. Also included in the invention is a method for identifying an islet cell precursor, the method involves analysing a cell for the expression of the Ngn3 gene product, where detection of the product is indicative of an islet cell precursor. The Ngn3 DNA sequence is useful as a diagnostic reagent for detecting (in a subject) a predisposition to a defect in pancreatic islet cell function or formation associated with a defect in Ngn3 activity. The Ngn3 protein is useful for identifying beta-cell precursor cells expressing Ngn3, and to alter cellular differentiation in culture in vivo to produce new beta-cells to treat patients with diabetes mellitus. The present sequence represents the murine Ngn3 genomic DNA
                                                                                                                                                                                                                                        The human neurogenin 3 Ngn3 DNA sequence AAC61089 encodes the Ngn3 protein AAY85617. The Ngn3 gene is located at chromosome position 10q22.1-22.2. The invention relates to the human Ngn3 nucleotide a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neurogenin 3; Ngn3; cellular differentiation; diabetes mellitus; islet cell precursor identification; mouse; ds.
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                                                                                                                                                                                                                                                                                                                        human neurogenin 3 polypeptides and polynucleotides encoding useful for diagnosis, prevention and treatment of diabetes tus and to identify individuals at risk of diabetes -
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                                                                                                                                                                                                                                                                                                                      CCATCCTATCTGCTCCCGGGAGCACTGGTGTTCTCAGACTTCTTG 1734
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                                                                                                                                                                                                                                                                                                                                                                                             GlySerLeuSerProAlaAlaSerLeuGluGluArgProGlyLeuLeuGlyAlaThrSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerAlaLeuAspAlaLeuArgGlyValLeuProThrPheProAspAspAlaLysLeuThr
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WO200073764-A2 Mus musculus.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid sequence, or any of its homologues or orthologues as therapeutic agents for the treatment of deafness, partial hearing loss, vestibular effects due to damage or loss of inner hair cells, osteoarthritis and abnormal cell proliferation. The invention also encompasses methods of screening for compounds which affect the expression of an atonal-associated nucleic acid sequence in an animal, and a transgenic animal in which an allele of a native atonal-associated gene is replaced by a heterologous nucleic acid sequence, thus inactivating the atonal-associated allele. The nucleic acids or proteins may be used in a method of treating an animal for hearing impairment, joint disease, balance disorders, abnormal cell proliferation, or other disease related to loss of a functional atonal-associated nucleic acid or protein. They may particularly be used to treat an animal with a deficiency in cerebellar granule neurons or their precursors, and may lead to treat an animal with a second to treat the second to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page -; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Therapeutic use of atonal-associated nucleic acids or amino acids, or any of its homologs or orthologs, for the treatment of e.g. deafness, osteoarthritis and abnormal cell proliferation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1999; 99US-0137060.
19-JAN-2000; 2000US-0176993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5567 BP; 1271 A; 1549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to the use of atonal-associated nucleic acid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-032190/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               o be used in promoting mechanoreceptive cell growth and generating r cells. The present sequence represents an atonal-associated nucleic d sequence referred to in the invention.

e: The present sequence is not shown in the specification, but obtained from GenBank.
                                                     5163
                                                                                                                                                    5103
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SerAlaLeuAspAlaLeuArgGlyValLeuProThrPheProAspAspAlaLysLeuThr
                                                                                                                                                                              LeuArgAlaArgArgGlyGlyArgSerArgProLysSerGluLeuAlaLeuSerLysGln
                                                                                                                                                                                                                                                                                                                                               TTTCCCGGAGCCTCGGACCACGAAGTGCTCAGTTCCAATTCCACCCCACCTAGCCCCACT
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                                                                                  ArgArgSerArgArgLysLysAlaAsnAspArgGluArgAsnArgMetHisAspLeuAsn
                                                                                                                                               CTCCGCGCCCGACGCGAGGGCGCAACAGGCCCAAGAGCGAGTTGGCACTCAGCAAACAG
                                                   CGAAGAAGCCGGCGCAAGAAGGCCAATGATCGGGAGCGCAATCGCATGCACCAACCTCAAC
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Indels:
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RESULT 11
ABQ49522/c
ID ABQ495
This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligomuclectides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The methor is used: (i) for diagnosis and/or prognosis of side effects of the two chasses is defected of a wide range of diseases, e.g. cancer, disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligonucleotide
                                                                                                                                                                                                                                                                                                                                        Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                                            Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA -
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05-SEP-2000;
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SNP; cell differentiation; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
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RESULT 12
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                                                                                           Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism SNP; cell differentiation; ds.
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This invention describes a novel method for determining the degree of cc methylation of a particular cytosine in a motif 5'-CpG-3', present in a cc genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic CC DNA that contains the target C is amplified to form a labeled amplicon. CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers CC and the degree of hybridisation to both classes is determined from the CC label on the amplicon. From the ratio of labels hybridised to two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory cof the central termining the degree of method allows the cutypes and for investigating cell differentiation. The method allows the cutypes and for investigating cell differentiation. The method allows the cutypes and for investigating cell differentiation of cell or tissue types and for investigating cell differentiation of cell or tissue types and for investigating cell differentiation of cell or tissue the method for determining the degree of cytosine methylation described in the disclosure of the invention.
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Sequence 592
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                                                                                                                                                            methylation of a particular cytosine in a motif 5'-CpG-3', present in a cytosine (c) but not methylated C, to uracil, then part of the genomic cytosine (c) but not methylated C, to uracil, then part of the genomic cytosine (c) but not methylated C, to uracil, then part of the genomic CC DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one contains the target C is amplified acid (PNA) oligomers and the degree of hybridiseation to both classes is determined from the calculated. The method classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory contents etc., particularly by detecting mutations or single nucleotide cypes and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously.
                                                               Sequence 592
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                                                                                                                                                                                                                                                                                                                                                                                                     Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                 Olek A,
                                                                                                                                                                    01-SEP-2000;
05-SEP-2000;
                                                                                                                                                                                                                                  01-SEP-2001;
                                                                                                                                                                                                                                                                              07-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide for detecting cytosine methylation
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Determining the degree of cytosine methylation in genomic DNA, useful
                                       WPI; 2002-371829/40
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                                                                                 Piepenbrock C,
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AB013410-AB054121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in
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AAF27264 standard; cDNA;

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3 ProGlnProSerGlyAlaProThrValGlnValThrArgGluThrGluArgSerPhePro

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CCAGCGCCCCCGACCGCCGACGGCC---

-ĠTĊGACCAGCGGCCGCGCCCCCTCTCCCC

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Best
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US-09-595-947E-10 (1-214) x AAF27264 (1-790)
                                                                           Query Match:
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                                                                                                                                                                                                                Alignment
                                                                                                                                                                                                                                                                                                                                                             The invention relates to the use of atonal-associated nucleic acid or CC amino acid sequence, or any of its homologues or orthologues as CC therapeutic agents for the treatment of deafness, partial hearing loss, CC vestibular effects due to damage or loss of inner hair cells, CC osteoarthritis and abnormal cell proliferation. The invention also CC encompasses methods of screening for compounds which affect the CC expression of an atonal-associated nucleic acid sequence in an animal, CC and a transgenic animal in which an allele of a native atonal-associated CC gene is replaced by a heterologous nucleic acid sequence, thus CC inactivating the atonal-associated allele. The nucleic acids or proteins CC may be used in a method of treating an animal for hearing impairment, CC joint disease, balance disorders, abnormal cell proliferation, or other CC grotein. They may particularly be used to treat an animal with a CC deficiency in cerebellar granule neuronal atonal-associated mucleic acid or promoting mechanoreceptive cell growth and generating CC also be used in promoting mechanoreceptive cell growth and generating CC hair cells. The present sequence represents an atonal-associated nucleic acid sequence referred to in the invention.
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                                                                                                      Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1999; 99US-0137060.
19-JAN-2000; 2000US-0176993.
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                                                                                                                                                                                                                                                                   Sequence
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647 GCCTGCACTTTATCGCCCGGCAGCCCCGCCGGCTCC 682	뭣
201 AlaCysLeuSerProGlySerLeuAlaPheSer 211	Ś
614 GGCGCCAGCCCCGCGCCCTCC	ఠ
181 SerLeuSerProAlaAlaSerLeuGluGluArgProGlyLeuLeuGlyAlaThrSerSer	8
584 AGCCCCTCGCCCGCCTCGTCGTGGAGCGGC	皮
161 SerProGlyGlyProProGlyAspTrpGlySerLeuTyrSerProValSerGlnAlaGly	Ş
524 GCCGGGGCCCGCCTGGGGGGCGCCGCCGACGCCCCGCGGGGGGCGGCCGAGGGC	皮
142 AlaAspHisSerLeuTyrAlaLeuGluProProAlaProHisCysGlyGluLeuGly	Ş
464 ATCGAGACGCTGCGCTTCGCCCACAACTACATCTGGGCGCTCACCGAGACGCTGCC	뮹
122 IleGluThrLeuArgPheAlaHisAsnTyrIleTrpAlaLeuThrGlnThrLeuArgIle	Ş
404 GCGCTGGACGCGCGACGTGCTGCCCACCTTCCCCGAGGACGCCAAGCTCACCAAG	문
102 AlaLeuAspAlaLeuArgGlyValLeuProThrPheProAspAspAlaLysLeuT	8
344 CGGAGCCGGCTGAAAGCCAACAACCGCGAGCGCAACCGCATGCACAACCTGAACGCG	ઠ.
82 ArgSerArgArgLysLysAlaAsnAspArgGluArgAsnArgMetHisAspLeuAs	. &
284 GGGCGGCAGCGAGGGCCCCCGCGGGGCGCGCACGGCGAGACGCCGC	뮹
67 GlyArgSerArgProLysSerGluLeuAlaLeuSerLysGlnArg	Ş
224 GAGGACGAGGACGAGGACGGCGGCGGCGGCGGCTGCAGGAGGGCGCTCGGCGGCG 283	皮
49 AlaGluGlyGlyCysArgGlyAlaProArgLysLeuArgAlaArgAr	Ş
164 CTGCTGCGCCTCGCCTCGCCCCCTCGGCCTCGCTGCCGTCCAGCGCCGGGAG	당
30 ThrCysProThrSerAlaProProSerProThrArgThrProGlyAsnCysAlaGlu	Ş
104 CGCCCCCGCAGGATGCCGGTGAAGGCGGAGAGCCCGGCGCGCCGCGGCGGAGGACGACTG	뮹
23 ArgAlaSerGluAspG	Ş

Search completed: February 2, 2004, 20:02:31 . Job time : 283 secs

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Run on:

OM protein - nucleic search, using frame_plus_p2n model

Copyright

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

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Result
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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
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                     Score
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Ygapop 10.0 , X
Fgapop 6.0 , I
Delop 6.0 , I
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4 US-10-004-717-30

4 US-10-004-717-37

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ALIGNMENTS

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Sequence 1, Application US/09817360

Patent No. US20020015696A1

GENERAL IMPORMATION:
APPLICANT: German, Michael S.
APPLICANT: German, Michael S.
APPLICANT: Lin, Joseph
TITLE OF INVENTION: PRODUCTION OF PANCREATIC ISLET CELLS
TITLE OF INVENTION: AND DELIVERY OF INSULIN
FILE REFERENCE: UCSF-129CIP
CURRENT APPLICATION UNMBER: US/09/817,360
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/535,145
PRIOR APPLICATION NUMBER: 60/128,180
PRIOR FILING DATE: 1099-04-06

PRIOR FILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1
LENGTH: 5340
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-817-360-1
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US-09-817-360-1
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APPLICANT: ZOGHBI, HUDA Y.
APPLICANT: YANG, QI
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF A
TITLE OF INVENTION: ATONAL ASSOCIATED SEQUENCE FOR DEAFNESS,
TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION
FILE REFERENCE: P01899US4
CURRENT APPLICATION NUMBER: US/10/004,717
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/585,645
PRIOR APPLICATION NUMBER: 60/176,993
PRIOR APPLICATION NUMBER: 60/137,060
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 2000-01-01
PRIOR FILING DATE: 1999-06-01
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Pred. No.:
                                                                                                                                                                                             Sequence 4, Application US/10004717 Publication No. US20020192665A1 GENERAL INFORMATION:
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RESULT 3
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SOFTWARE: PatentIn Ver. :
SEQ ID NO 4
                                                                                                          Sequence 24, Application US/10004717 Publication No. US20020192665A1 GENERAL INFORMATION:
APPLICANT: ZOGHBI, HUDA Y.

APPLICANT: YANG, QI

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE
TITLE OF INVENTION: ATONAL ASSOCIATED SEQUENCE FOR DEAFNESS,
TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION
FILE REFERENCE: P01899US4
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; LENGTH: 861
; TYPE: DNA
; ORGANISM: Mus musculus
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CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/585,645
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: 60/176,993
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: 60/137,060
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PATENTIN Ver: 2.1
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CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/35,145
PRIOR FILING DATE: 2000-03-24
PRIOR PRIOR DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 60/128,180
PRIOR FILING DATE: 1999-04-06
PRIOR APPLICATION NUMBER: 00/128/145
PRIOR A
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APPLICANT: Lin, Joseph
TITLE OF INVENTION: PRODUCTION OF PANCREATIC
TITLE OF INVENTION: AND DELIVERY OF INSULIN
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ORGANISM: Mus
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; ORGANISM: chicken
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LENGTH: 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/137,060 PRIOR FILING DATE: 1999-06-01 NUMBER OF SEQ ID NOS: 69
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PRIOR TILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: 60/176,993
PRIOR FILING DATE: 2000-01-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF TITLE OF INVENTION: ATONAL ASSOCIATED SEQUENCE FOR DEAFNESS,
TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION
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CURRENT FILING DATE: 2002-08-16
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APPLICANT: ZOCHBI, HUDA Y.

APPLICANT: YANG, QI

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF APPLICANT: YANG, ATONAL ASSOCIATED SEQUENCE FOR DEARNESS,
TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION
FILE REFERENCE: POLOSYUSA

CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US/10/004,717
CCURRENT FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: 60/137,060
PRIOR FILING DATE: 2000-06-01
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Oy 150 GluproproAlaProHisCysGlyGluLeuGlySerProGlyAlyProProGlyAspTrp 169 Db 952 CTGAGCCCGGGAGCCTGGGCCCAGGGGCAGGGGCCAGGCCCTTCCCCCTCT	Db 538 GGGCAGCGGAAGCCGAAGCCGAAGCCGAGGCAGGCAGTCCGGGTTCCGGGTGCCGGG 597 Qy 53 GlyCysArgGlyAlaProArgLysLeuArgAla

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                                                                                  Sequence 37, Application US/10004717 Publication No. US20020192665A1 GENERAL INFORMATION:
APPLICANT: ZOGHBI, HUDA Y.

APPLICANT: YANG, QI
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE
TITLE OF INVENTION: ATONAL ASSOCIATED SEQUENCE FOR DEAFNESS,
TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION
FILE REFERENCE: P01899US4
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CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/585,645
PRIOR FILING DATE: 2000-06-01
PRIOR PILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: 60/176,993
PRIOR APPLICATION NUMBER: 60/17,060
PRIOR APPLICATION NUMBER: 60/137,060
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 37
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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RESULT 10
US-08-722-570-12
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Publication NO. US20030044887A1
GENERAL INFORMATION:
APPLICANT: Anderson, David J.
APPLICANT: Ma, Qiufu
TITLE OF INVENTION: NEUROGENIN
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1527 base pairs
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                                                                                                                                                                                                                                                                                                                        Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
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NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,570
FILING DATE: 27-SEP-1996
FILING DATE: 27-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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TOPOLOGY: un
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
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    CCCTCTCCGGGGCATCGAACGTTCCCGGTGGCCAGGACGAAGAGCAGGAG---
                                                                                GGCTCCAGCCCTAGCTTCCACCTCAGGGCTGTCCGTGCCAGCCCGCAGGAGCGCGCCCA
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                                         ProSerPro---ThrArgThr--ProGlyAsnCysAlaGluAlaGluGluGlyGlyCysA 55
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US-08-722-570-13
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                                                   TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
LENGTH: 738 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/08722570
Publication No. US20030044887A1
GENERAL INFORMATION:
APPLICANT: Anderson, David J.
                                                                                                                                                                       PILING DATE: 27-SEP-1966
CLASSIFICATION: 5365
ATTORNEY/AGENT INFORMATION:
NAME: S11va, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-63
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TOPOLOGY: u
                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/722,57/FILING DATE: 27-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ma, Qiufu
TITLE OF INVENTION: NEUROGENIN
NUMBER OF SEQUENCES: 20
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                                     STRANDEDNESS:
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Percent Similarity:
Best Local Similarity:
Query Match:
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US-08-722-570-14
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                                                                                                                                                                                                                                             Sequence 14, Application US/08722570 Publication No. US20030044887A1 GENERAL INFORMATION:
                                                                                                                                                    APPLICANT: Anderson, David J.
APPLICANT: Ma, Qiufu
TITLE OF INVENTION: NEUROGENIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                     ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                       STATE: C
                                                                                                         STREET: Four Embarca
CITY: San Francisco
                                                                                                                                           ADDRESSEE:
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                                                                         United States
                   Floppy disk
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REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-63
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEFX: 910 277299
INFORMATION FOR SEQ ID NO: 14:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,570
FILING DATE: 27-SEP-1996
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LENGTH: 1312 base pairs
TYPE: nucleic acid
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                                                                                                                                                            CGACCCAGTGCACCGATCTGCTTCCACCCCAGCAGCAGCCATATTGGTGCAGGACTCCTC
                                                                                                                                                                                           aAspHisSerLeuTyrAlaLeuGluProProAlaProHisCysGlyGluLeuGlySerPr 162
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Conservative:
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Indels:
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Query Match:
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APPLICANT: Anderson, David J.
APPLICANT: MA, Qiufu
TITLE OF INVENTION: NEUROGENIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1277 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
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CORRESPONDENCE ADDRESS:
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REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
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                                                                                              ArgArgGlyGlyArgSerArgProLysSerGluLeuAlaLeuSerLysGlnArgArgSer 83
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RESULT 14
US-10-004-717-43
US-10-004-717, Sequence 43, Application US/10004717
; Publication No. US20020192665A1
; GENERAL INFORMATION:
; APPLICANT: ZOGHEI, HUDA Y.
; APPLICANT: YANG, QI
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SEQ ID NO 43
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CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/585,645
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: 60/176,993
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 2000-01-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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AGAAAGTTTGCTAGACAATGTGAGGACCAGAAACAAATTAAGAAACCAGAGAGCTTTCCA
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                                                                       AAACAAGTTGTCCTTCGAGGAAAGAGCATTAAAAGGGCCCCCTGGAGAAGAAACCGAGAAA
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Score:
Best Local Similarity:
Query Match:
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                                 Percent Similarity:
                                                                   Alignment Scores: Pred. No.:
                                                                                                                                                   SEQ ID NO 8
LENGTH: 1957
TYPE: DNA
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Publication No. US20020192665A1
GENERAL INFORMATION:
                                                                                                                     ORGANISM: Mus musculus -10-004-717-8
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APPLICANT: YANG, QI
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE
TITLE OF INVENTION: ATONAL ASSOCIATED SEQUENCE FOR DEAFNESS,
TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION
FILE REFERENCE: PO1899US4
CURRENT APPLICATION NUMBER: US/10/004,717
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/585,645
PRIOR FILING DATE: 2000-06-01
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FILING DATE: 2000-01-19
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                               LeuLeuGlyAlaThrSerSerAlaCysLeuSerPro 205
                                                                                              SerProValSerGlnAlaGlySerLeuSerProAlaAlaSerLeuGluGluArgProGly 193
                                                                                                                                 TACCACAGCCCTGAGCTGGCCACTCCCCCAGGG-----
                                                                                                                                                              ProHisCysGlyGluLeuGlySerProGlyGlyProProGlyAspTrpGlySerLeuTyr 173
                                                                                                                                                                                                                                                                 CAGCCAACTACAAACTTGGTGGCAGGCTGCTTACAGCTCAACGCCAGAAGTTTCCTGATG
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Search completed: February 2, 2004, 21:41:42
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-Q2/Cgn2 1/USPTO spool/US09595947/runat 02022004 154934 8059/app query.fasta_1.391
-DB=EST -QFMT=fastap -SUFFIX-rst -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bite -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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-NO_MMAD -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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SUMMARIES

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ALIGNMENTS

RESULT 1 AK008017 LOCUS DEFINITION

AK008017.1 GI:12841941 HTC; CAP trapper. Mus musculus (house mouse) AKOO8017

1540 bp mRNA linear HTC 05-DEC-2002 Mus musculus adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010001M19 product:atonal homolog 5 (Drosophila), full insert sequence. AK008017

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Mus musculus Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.

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REFERENCE
AUTHORS
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Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome
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                                                                                                             Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rot = 20.0. Se of sequence[5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Please visit our web site (http://genome.gsc.riken.go.jp/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax:81-45-503-9216)
                                                                           ArgThrProGlyAsnCysAlaGluAlaGluGluGlyGlyCysArgGlyAlaProArgLys 60
                                                                                                                                                                                                                                 MetThrProGlnProSerGlyAlaProThrValGlnValThrArgGluThrGluArgSer
LeuArgAlaArgArgGlyGlyArgSerArgProLysSerGluLeuAlaLeuSerLysGln 80
                                          CTCATACCTAGGGACTGCTCCGAAGCAGAAGTGGGTGACTGCCGAGGGACCTCGAGGAAG
                                                                                                                                                                 PheProArgAlaSerGluAspGluValThrCysProThrSerAlaProProSerProThr 40
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/db_xref="GI:12841942"
/db_xref="GI:12841942"
/db_xref="MGI:893591"
/translation="MAPHPLDALTIQVSPETQQPFPGASDHEVLSSNSTPPSHTLIPR
/CSEAEVGDCRGTSRKLRARRGGRNRPKSELALSKKRRSRRKKANDREENRMHNINSA
LDALRGVLPTFPDDAKTKVETLRFAHNYIWALTQTIRIADHSLYGPEBPVPCGELGS
PGGGSNGJWGSIYSPVSQAGNLSPTASLEEFPGLQVPSSPSYLLPGALVFSDFL"
a 485 c 397 g 352 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue type="small intestine"
/clone_lib="RIKEN full-length
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="unnamed protein product; atonal homolog 5 (prosophila) (MGD|MGI:893591, GB|NM_009719, evidence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="FANTOM_DB:2010001M19"
/db_xref="MGI:1907403"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'mol_type="mRNA"
'strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"
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JOURNAL
                                                                TITLE
                                                                      Nikaido, I., (Satto, N., Saito, R., Sutuki, H., Yamanaka, I., Kyosawa, H., Nikaido, I., (Satto, N., Saito, R., S., Nogami, A., Schonbach, C., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C.F., Forrest, A., Frazer, K. S., Gassterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hitokawa, N., Jackson, I.J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., Gough, J., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Marchionni, L., McKenzie, L., Miki, P. R., Maglott, D. R., Marchionni, L., McKenzie, L., Miki, Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Redd, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Walls, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Arakawa, T., Forno, H., Nakamura, K., Sakazume, N., Sato, K., Shinada, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y., Sasaki, D., Shibata, K., Sasaki, D., Shibata, K., Shipata, F., Paralyonis, G., Finchishi, A., Sakai, M., Waterston, R., Lander, J., Barney, E. and Hayashizaki, Y., Sasaki, D., Shibata
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                       Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kasukawa, T., Adachi, J., Bono, H.,
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Length: Matches: Mismatches: Conservative:

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Score: Pred. No.:

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URL:http://genome.gsc.riken.go.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Hori,F., Imotani,K.,
S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K.,
Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno
H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
Numazaki,R., Ohno,M., Ohasto,N., Saito,R., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Recommendation of the sequencer of the sequenc
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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           215
/note="Site 1: XhoI; Site 2: SstI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
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/dev_stage="adult"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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RPCI-23-160G18.TV RPCI-23 Mus
                                                 Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                          Other_GSSs: RPCI-23-160G18.TJ
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Mouse BAC End Sequences from Library RPCI-23
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            GlyGlyProProGlyAspTrpGlySerLeuTyrSerProValSerGlnAlaGlySer 181
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Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
library availability, please contact Pieter de Jong
pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetizs (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
plate: 160 row: G column: 18
/ Bex= remain | Claim 
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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kidney and/or
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US-09-595-947E-10 (1-214) x AZ296526 Similarity: ProGlnProSerGlyAlaProThrValGlnValThrArgGluThrGluArgSerPhePro 3.96e-37 676.50 82.68% 75.98% 60.03% (1-593)Length: Matches: Conservative: Gaps: Mismatches: Indels: 593 136 12 30 2

ArgAlaSerGluAspGluValThrCysProThrSerAlaProProSerProThrArgThr LeuAspAlaLeuArgGlyValLeuProThrPheProAspAspAlaLysLeuThrLysIle GCCCGACGCGGAGGGCCCAACAGGCCCAAGAGCGAGTTGGCACTCAGCAAACAGCGAAGA AlaArgArgGlyGlyArgSerArgProLysSerGluLeuAlaLeuSerLysGlnArgArg ProGlyAsnCysAlaGluAlaGluGluGlyGlyCysArgGlyAlaProArgLysLeuArg GGAGCCTCGGACCACGAAGTGCTCAGTTCCAATTCCACCCCACCTAGCCCCACTCTCATA 428 AspHisSerLeuTyrAlaLeuGluProProAlaProHisCysGlyGluLeuGlySerPro 162 GAGACCCTGCGCTTCGCCCACAACTACATCTGGGCACTGACTCAGACGCTGCGCATAGCG GluThrLeuArgPheAlaHisAsnTyrIleTrpAlaLeuThrGlnThrLeuArgIleAla CTGGATGCGCTGCGCGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAGATC SerArgArgLysLysAlaAsnAspArgGluArgAsnArgMetHisAspLeuAsnSerAla CCTAGGGACTGCTCCGAAGCAGAAGTGGGTGACTGCCGAGGGACCTCGAGGAAGCTCCGC GACCACAGCTTCTATGGCCCGGAGCCCCCTGTGCCCTG----GGAGAGCTGGGGAGCCCC AGCCGGCGCAAGAAGGCCAATGATCGGGAAGCGCAATCGCACGAACCTCAACTCGGCG 42 142 122 102 128 188 308 82 368 62 488 22 248 72

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Tissue Procurement: Dr. David Rowe and Dr. Mina
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
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AGENCOURT 11295215 NIH MGC 164 Mus
IMAGE:30146192 5', mRNA sequence.
CA979119
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High quality sequence start: 16
High quality sequence stop: 640.
Location/Qualifiers
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Mammalia; Eutheria; Rodentia;
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CA979119.1 GI:27511773
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National Institutes of Health, Mammalian Gene Collection (MGC)
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1 (bases 1 to 932)
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                      CCAGCTTCCTCACCGACGAGGAGGACT---GTGCCAGGCTACAGCCCCTA-GCCTCCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:1090"
/db_xref="taxon:1090"
/clone="IMAGE:30146192"
/lab_host="DH10B (phage-resistant)"
/clone="lb="NHH MGC 164"
/clone="lb="NHH MGC 164"
/clone=lb="NHH MGC 164"
/note="Vector: pCMV-SPORT6.1.ccdb; Site_1: EcoRV; Site_2:
NotI; Non-normalized full-length enriched library from pooled mouse embryonic limb, maxilla and mandible, day 10.5 and 11.5 (size selected for the 0.5-1 kb fragments)
Cloned directionally, priming method: Oligo-dT. cDNA enrichment: >lk bp, Average insert size 1.8k bp. Priming sequence: 5'GACTAGTTCTAGANTCGCGACCGCCCC(T) 3'. Tissue contributed by, David Rowe. Library constructed by ResGen, Invitrogen Corp."
153 a 349 c 276 g 153 t 1 others
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Leonard I. Zon,
                                                                                                                                                                                                                                                                                                            i (bases 1 to 865)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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IMAGE: 6789795 5', mRNA sequence.
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Actinopterygii; Neopterygii; Teleostei;
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                                                                                                                                                                cDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
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                                                                                            quality sequence stop:
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/mol_type="mRNA"
/db_xref="taxon:7955"
                                                                         Location/Qualifiers
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/lab host="PH108 (T1-resistant)"
/lab host="NCI (GAP_ZEMb2"
/clone_lib="NCI (GAP_ZEMb2"
/note="Vector: pCMV-SPORT6.ccdb; Site_1: EcoRV; Site_2: /note="Vector: pCMV-SPORT6.ccdb;
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Email: thisse@igbmc.u-strasbg.fr
EST from a cDNA of a gene whose expression is spatially restricted
during embryogenesis. We have established its expression pattern
during embryonic development by whole mount in situ hybridization
on zebrafish embryos from the gastrula stage to 2 days of
development. The corresponding data available on the zebrafish
community database at http://zfin.org/ cDNA library preparation: B.
Riggleman. DNA Sequencing by:IGBMC sequencing facility. Clone
Riggleman. DNA Sequencing by:IGBMC sequencing facility. Clone
distribution: zebrafish international resource center at the
University of Oregon (Institute of Neuroscience, 1254 University of
Oregon, Eugene, OR 97403-1254)
Seq primer: TA ATTAACCCTCACTAAAGGGA.
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Danio rerio (zebrafish)
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Institut de Genetique
CNRS, INSERM, ULP
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/note="Vector: Lambda Zap; Site_1: EcoRI; Site_2: XhoI;
/note="Twector: Lambda Zap; Site_1 corn RNA pooled from Oligo dT cDNA library constructed from RNA pooled from segmentation stage zebrafish embryos"
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Plate: 14108 row: O
High quality sequence
                                                                                                                                                                                                                                                                                                                                                                         Email: fchen@exelixis.com
DNA Sequencing by: Exelixis, Inc.
can be found through the I.M.A.G.
                                                                                                                                                                                                                                                                                                                                                                                                                            170 Harbor Way, PO Box
Tel: 650 837 7000
Fax: 650 837 8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Chen F.
Exelixis, Inc.
170 Harbor Way,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amundeen,C., Cachuela,N., Chen,F., Cheung,L.M., Chong,A., Oliva,J., Park,C., Reyes,J., Yungen,J. and Swimmer,C. Expressed sequence tags from NCI_CGAP_ZEmb2, a Danio rericembryonic library
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                                              /clone="IMAGE:6521499"
/tissue_type="embryo"
/lab_host="PHIOB (TI-resistant)"
/lab_host="PHIOB (TI-resistant)"
/clone_lib="NCI_GAP_ZEmb2"
/clone_lib="NCI_GAP_ZEmb2"
/note="Vector: pCMV-SPORT6.ccdb; Site_1: BcoRV; Site_2:
NotI; Cloned_unidirectionally. Primer: Oligo dT. Average
insert_size_2 kb. Constructed by J. Wang (Research
insert_size_2 kb. Constructed by J. Wang (Research
Genetics, Invitrogen Corp) from tissue donated by L. Zor
(Harvard_University). Note: this is a NCI_CGAP_Library.'
a 185 c 155 g 104 t
                                                                                                                                                                                                                             /organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
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Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
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Oryzias latipes
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Medaka EST Project in Takeda's lab
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CA945402 687 bp mRNA linear EST 30-DEC-2002 UI-M-FDO-cdh-l-12-0-UI.rl NIH_BMAP_FDO Mus musculus cDNA clone
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Location/Qualifiers
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/sex="mixture of female and male"
/tissue_type="whole embryo"
/dev_stage="segmentation stage 20 -
/clone_lib="MF01SSA_CDNA"
/clone_lib="MF01SSA_CDNA"
10 g 90 t 1 c
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317.50
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Best Local Similarity:
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Tissue Procurement: Dr. James Lin, Univeristy of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University ocDNA Library Arrayed by: Dr. M. Bento Soares, University of DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LinL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST.
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CA945402
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NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                       GluThrGluArgSerPheProArgAla----
                                                                       CTGATGCTGCTGGGCTCGGCTTCCCCGGGCCTCGGCCGACCCTGACCCCGATGTCCTCCAGC 196
                                                                                                                                                              GAGCCGCGTAGGATGTTCGTCAAATCTGAGACTCTGGAGTTGAAGGAGGAAGAGGAGGTA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer: pYX-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="whole brain"
//dev stage="wembryo 12.5 dgpc"
/lab_host="MIHDB (TI phage resistant)"
/clone_lib="WIH_BMAP_FDO"
/clone_lib="WIH_BMAP_FDO"
/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
/note="Torgan: brain; Vector: pXX-Asc; Site_1: EcoR I;
/note="Torgan: brain; Vector: brain; Vector: pXX-Asc; Vector: brain; Vec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE: 6828925"
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Sciurognathi; Muridae;
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COMMENT
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AUTHORS
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                                                                                                                                                                  sequence.
Plate: 0016
Seq primer: N
                                                                                                                                                                                                        Fax: 02.23.48.50.20 Email: Yann.Guiguen@beaulieu.rennes.inra.fr Sequence cleaned of vector, adaptator and reat sigenasupport@jouy.inra.fr to obtain the
                                                                                                                                                                                                                                              Campus de beaulieu,
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence.
BX308104
BX308104.1 GI:29588749
EST
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BX308104 AGENAE Rainbow trout
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INRA - SCRIBE
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Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus
                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                         Oncorhynchus mykiss
                                                                                                                                                                                                                                                                                                                            Construction and primary characterization of normalized libraries in rainbow trout, Oncorhynchus mykiss
                                                                                                                                                                                                                                                                                                                                                      Govoroun, M., Guiguen, Y. and Le Gac, F.
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                                               /tissue_type="adipose tissue, blood, brain, differentiating gonads, gills, interrenal, intestine kidney, liver, muscle, ovary, pituitary, testis"
                                                                                        /clone="tcay0016b.k.15"
                                                                                                   organism="Oncorhynchus
/mol_type="mRNA"
/db_xref="taxon:8022"
                                                                                                                                                      Location/Qualifiers
                         /dev_stage="from embryos to adults"
/lab_host="DH10B"
                                                                                                                                             . 604
                                                                                                                                                                              row: k
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lib="AGENAE Rainbow trout (tcay)"
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Percent Similarity:
Best Local Similarity:
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                                                                                                                 203 GATGACGAAGATTCGTGCAGCAGCATGCACGCTTCCTCCCCTTCATCCTCCATCGGCAAG
                               Department of Biochemistry and Molecular Biology University of Texas M.D. Anderson Cancer Center Box 117, 1515 Holcombe Blvd., Houston, TX 77030, Tel: 713 792 3646
                                                                                                                                                                                                                                                                                                                                                                                        BG808248
2083-52 Mouse
                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                   Contact: Klein WH
                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                          BG808248.1
                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence
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Francois.Piumi@jouy.inra.fr, INF
Etude du genome (IREG), Domaine
Jouy-en-Josas cedex, FRANCE"
a 178 c 148 g 116 t
Location/Qualifiers
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BU924937
BU924937.1 GI:
EST.
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Contact: Klein WH
Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030,
Tel: 713 792 3646
                                                                                              Nucl
                                                                                                                    Mu,X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarp. White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. Gene expression in the developing mouse retina
                                                                                                                                                                                                                                                                                BU924937
7103-91 Mouse E14.5
                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 600)
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                                                                                                         and microarray analysis
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/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="neural retina"
/dev_stage="embryonic day 14.5 pour clone_lib="Mouse_E14.5 retina late 238 c 161 g 107 t
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Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                  mouse)
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retina lambda
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; Murinae; Mus
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CSODF035YD19 5-PRIME, m
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/dev_stage="embryonic day 14.5
/clone_lib="Mouse_El4.5 retina
/clone_122 g 82 t
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'db_xref="taxon:10090"
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FETAL BRAIN Homo
mRNA sequence.
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Conservative:
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was not normalized. Library was constructed by Life Technologies,
division of Invitrogen. This sequence belongs to sequence cluster
2626.r, Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODF035CB10QP1.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                    ArgGlyValLeuProThrPheProAspAspAlaLysLeuThrLysIleGluThrLeuArg
                                                                   AGGCCAACAACCGCGAACCGCAACCGCATGCACAACCTCAACGCGGCACTGGACGCGCTG
                                                                                                                                         GTCTCCCGAGGCGCCAAGACGGCCGAGACGCTGCAGCGCATCAAGAAGACCCCTAGACTG
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   CGCGAGGTGCTCCCCACGTTCCCCGAGGACGCCAAGCTCACCAAGATCGAGACMCTGCGC
                                                                                         LysAlaAsnAspArgGluArgAsnArgMetHisAspLeuAsnSerAlaLeuAspAlaLeu
                                                                                                                                                                            LeuSerLysGln--
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/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and ECORV sites of the pCMVSPORT 6
vector. Library was not normalized."

322 c 342 g 121 t 26 others
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/db_xref="taxon:9606"
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/tissue_type="FETAL BRAIN"
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/mol_type="mRNA"
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Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     601469349F1 NIH_MGC_67 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                             PheProArgAlaSerGluAspGluValThrCys-----
                                                                 CAGCCCGCCTTGAGACCTGCATCTCCGACCTCGACTGCGCCAGCAGCAGCAGCAGCAGTGACC
                                                                                                GlnProSer-----GlyAlaProThrValGlnValThrArgGluThrGluArgSer 20
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                                                                                                                                                                                                                                                                                                                       228
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                                                                                                                                                                                                                                                                                                                                  /tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 67"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned uniddrectionally. Primer: Oligo Average insert size 1.75 kb. Library constructed by Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mol_type="mRNA"
db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
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IMAGE:3872172 5',
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                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@ulowa.edu
This clone was contributed by the Brain Molecular Anatomy Project
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BU612495.1 GI:23278710
EST.
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UI-M-FRO-cbc-k-21-0-UI.rl NIH BMAP_FRO Mus
UI-M-FRO-cbc-k-21-0-UI 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 730)
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National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
                                                                                                                                                                                                         (BMAP)
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                                                                                                                                                                       primer: pYX-5
/mol_type="mRNA"
/strain="C57BL/6"
                                                                                                                                    Location/Qualifiers
                                                                    organism="Mus musculus"
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SUMMARIES

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1491 bp Sequence 1 from Patent WO9827206. A91167 Rattus sp. Rattus sp. Rattus sp. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Rammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; DNA

linear

PAT 22-JAN-2000

ALIGNMENTS

ACCESSION VERSION KEYWORDS

A91167.1

SOURCE

ORGANISM

RESULT 1
A91167
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REFERENCE AUTHORS

Rattus.

1 (bases 1 to 1491)
Icard-Liepkalns,C., Mallet,J. and Corresponding,N.A.
Patent: WO 9827206-A 1 25-JUN-1998;

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Liepkalns, C.I., Mallet, J. and Ravassard, P.

Polypeptide belonging to the family of basic helix-loop-helix

(bHLH) family and nucleic acid sequence corresponding thereto

Patent: JP 200151-0464A 1 31-JUL-2001;
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PI CHRISTINE ICARD LIEPKALMS, JACQUES MALLET, PHILIPPE RAVASSARD CO7K14/47, A61K31/711, A61K35/76, A61K38/00, A61K48/00, A61P25/00, PC C12N15/00, A61K37/02
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CC Topology: Linear:
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 GTGTCCTGCCCACCTTCCCCGGATGACGCCCAAACTTACAAAGATCGAGACCCTGCGCTTCG
                                      CCAACGACCGGGAGCGCAACCGCATGCACAACCTTAACTCCGCGCTGGATGCGCTGCGCG
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/db_xref="taxon:10118"
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R. norvegicus mRNA for transcription y10619

Y10619.1 GI:2072737

Relax; transcriptional regulator.
Rattus norvegicus (Norway rat)

Mammalia; Eutheria; Rodentia; Sciun
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REFERENCE AUTHORS TITLE Ravassard, P., Chatail, F., Mallet, J. and Ica Relax, a novel rat bHLH transcriptional reg expressed in the ventricular proliferating central nervous system J. Neurosci. Res. 48 (2), 146-158 (1997) Rattus

ORGANISM

Craniata; Vertebrata; Sciurognathi; Muridae;

Euteleostomi;
Murinae;

Icard-Liepkalns,C
regulator transiently

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AUTHORS
TITLE J. Neurosci. 97276390

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Ravassard, P.
Direct Submission
Submitted (20-JAN-1997) P. Ravass
Hopital de la Pitie Salpetriere, Ravassard, C riere, 83 Bd. CNRS UMR 9923, 1

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DCSEAEAGDCRGTSRKLRARRGGRNRPKSELALSKQRRSRRKKANDRERNRMHNLNSA
LDALRGVLPTPPDDAKLTKLETLRFAHNYIWALTQTLRIADHSFYGPEPPVPCGELGS
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                                                                                                              HTG; HTGS_PHASE1; HTGS_DRA
Rattus norvegicus (Norway
                                                                                                                                     AC127817
AC127817.3 GI:25077905
                                                                                                     Rattus norvegicus
                                                                                                                                                                       Rattus norvegicus clone
                                                                    Rattus.
                                                                                         Eukaryota; Metazoa;
                                                                                                                                                          unordered pieces.
                                                                                                                                                                                  AC127817
                                                                             Mammalia; Eutheria;
                                                                                                                                                                                                                                                    AGAGTGACCTAATCCAGTGT
                                                       (bases 1 to 258815)
                                                                              Chordata;
Rodentia;
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GCTGTGCGTGCACAAAGGATATTGCAGGCTGATCTCCTCTTAACCCTCCTCAGTGTGGCC
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                                                                                                                         ACCTCAAACTCCCGCTCCAAGCAGGAGGAGCCGTAGCACTAAATAGTTGGGAGACTCCC
                                                                                                                                                                                                                                                                                                                                   CCCTTCTGGCTTTCATTAGTCAGGTCCCTGATTTAACCAGGATTCGCACAGTTCCTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                    AAAGGGAGGGAGTCAGAGCTGTCTGAAATGGAAGGTAGTGGAGGCACTCGAGCATCTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGAGGAGTTCCCTGGCCTGCAGGTGCCCAGCTCCCCATCCTGTCTGCTCCCGGGCACCC
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ATACTTCCTGGTGACTCCGCCCTCTTTCAAATCTGCGGGCCTCCAACCACCGCTTTCTCC
                         ATACTTCCTGGTGACTCCGCCCTCTTTCAAATCTGCGGGCCTCCAACCACCGCTTTCTCC
                                                                                               ACCTCAAACTCCCGCTCCAAGCAGAGGAGAGCCGTAGCACTAAATAGTTGGGAGACTCCC
                                                                                                                                                                                                                                                                                                    CCCTTCTGGCTTTCATTAGTCAGGTCCCTGATTTAACCAGGATTCGCACAGTTCCTTGCT
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Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, 258815 bp DNA lir le CH230-259G16, WORKING _DRAFT; HTGS_FULLTOP Craniata; Vertebrata; Sciurognathi; Muridae; Adams, C., DRAFT ad,M., Benahmed,F., Brown,M., Euteleostomi;
; Murinae; HTG 19-NOV-2002 SEQUENCE, 3 Alder, J.,

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Bryant, M., Buhay, C., Burch, P., Burcell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Cesar, H., Center, A., Chu, J., Chardenas, V., Chare, K., Cavazos, I., Cesar, H., Center, A., Chen, J., Ch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Bstimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 3 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
AAACTTCGAAGCGAGAGAGGGTTCAGCTATCCACCGCTGCTTGACCTCTGACC-ACCCG
                                                                                      GAGCTTCTTTGCTGCCTCCAGACGCAATTTACTCCAGGCGAGGGCGCCTGCAGCTCAGCA
                                                                                                                                                                                                                                GCCCGGCAGGCACGCTCCTGGTCCGGGCAGAGCAGATAAAGCGTGCCAGGGGCACACACG
                                                                                                                                                                                                                                                             GCCCGGCAGGCACGCTCCTGGTCCGGGCAGAGAGATAAAGCGTGCCAGGGG-ACACACG
                                                                                                                                                                                                                                                                                                                GGGCTCGCGTGGCGCAGTCCCTGGGCCCCCGTTGCTGATTGGCCCCGTGGCACAGGCAGCA
                                                                                                                                                ATTAGCAGCTCAGAAATCCCTCTGGGTCTCACCACTGCACAGAGGCCGAGGACCCCCTCC
                                                                                                                                                                      ATTAGCAGCTCAGAAGTCCCCTCTGGGTCTCACCACTGCACAGAGGCCGAGGAGCCCCCCTCC
                                                                                                                                                                                                                                                                                                                                                       GGTAGCGAGAGGAGCAGTCCCTGGGCCCCCGTTGCTGATTGGCCCCGTGGCACAGGCAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        255980
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257450
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Consensus quality: 224/47 bases at least Q40
Consensus quality: 227961 bases at least Q30
Consensus quality: 227952 bases at least Q30
Estimated insert size: 228243; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: GZXS
Center clone name: CH230-259G16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  end_sequence:BZ169378"
a 56888 c 58131 g 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone_end:T7
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/note="clone_boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone_end:Sp6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'db_xref="taxon:10116"
'clone="CH230-259G16"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence:BZ169379"
                                                                                                                                                                                                                                                                                                                                                                                                                  96.4*;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1407;
Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27624 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAACAGGCCCAAGAGCGAGTTGGCACTGAGCAAGCAGCGACGAAGCCGGCGCAAGAAGCC 248122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAACAGGCCCAAGAGCGAGTTGGCACTGAGCAAGCAGCGACGAAGCCGGCGCAAGAAGGC 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCAGAAGCAGGTGACTGCCGAGGGACATCGAGGAAGCTCCGTGCGCGGCGCGGAGGGCG 248062
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                             CCTCAAACTCCCGCTCCAAGCAGAGGAGGAGACCGTAGCACTAAATAGTTGGGAGACTCCCA 1381
                                                                                                                                                                                                                                                                                                                                                                                            AAGGGAGGGAGTCAGAGCTGTCTGAAATGGAAGGTAGTGGAGGCACTCGAGCATCTCGCC 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTGTTCTCAGACTTCTTGTGAAGGGCCCAAACAGGCCCTGGGCGGTGGGCGCTGGCAGA 1141
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CCTCAAACTCCCGCTCCAAGCAGAGGAGAGCCGTAGCACTAAATAGTTGGGAGACTCCCA
                                                                                                                                          CTGTGCGTGCACAAAGGATATTGCAGGCTGATCTCCTCTTAACCCTCCTCAGTGTGGCCA 1321
                                                                                                                                                                                                                                                             CCTTCTGGCTTTCATTAGTCAGGTCCCTGATTTAACCAGGATTCGCACAGTTCCTTGCTG 1261
                                                                                                             CTGTGCGTGCACAAAGGACATTGCAGGCTGATCTCCTCTTAACCCTCCTCAGTGTGGCCA
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SOURCE
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                                                                                                                                                                                                                                                                                                      Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 212279 bases at least Q40
Consensus quality: 213137 bases at least Q30
Consensus quality: 213137 bases at least Q30
Consensus quality: 213590 bases at least Q20
Insert size: 192000; agarose-fp
Insert size: 217944; sum-of-contigs
Quality coverage: 11.89 in Q20 bases; agarose-fp
Quality coverage: 10.54 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Direct Submission
Submitted (15-JUL-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus chromosome UNK clone RP23-459M2, WORKING DRAFT SEQUENCE, 7 unordered pieces.
AC127417
AC1274172 GI:24137619
HTG; HTGS_PHASE1; HTGS_PRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: M13; 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (19-OCT-2002) Genome Sequencing Center, 4444 For Parkway, St. Louis, MO 63108, USA
On Oct 19, 2002 this sequence version replaced gi:21759524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parkway, St. Louis, MO 63108, USA 3 (bases 1 to 215050) McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 215050)
McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McPherson, J.D. and Waterston, R.H. The sequence of Mus musculus clon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 215050)
McPherson, J.D. and Wat
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGTGACCTÁATCCAGTGT 1460
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  4228
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16590
16690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vector:
4227: contig of 4227 bp in length
4327: gap of unknown length
16589: contig of 12262 bp in length
16689: gap of unknown length
27318: contig of 10629 bp in length
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FEATURES
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Best Local Similarity 83.9%;
Matches 1275; Conservative
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   CCCAAGAGACCCAGCAACCCTTTCCCGGAGCCTCGGACCACGAAGTGCTCAGTTCCAATT 558
                                                                                                                                    GCGTACTCTAGTCCCGCGTGGAGTGACCTCTAAGTCAGAGACTGTCACACCCC--CCTTC 438
                                                                                                                                                                                                               ACTAGGTAACATTTAGGAACCTCCAAAGGGTAGAAGAGGGGAGTG------GGTGG 380
                                                                                                                                                                                                                                                                    TATCCACTGCTTGTCACTGACTGACCTGCTCTCTATTCTTTTGAGTCGGGAG-A
                                                                                                                                                                                                                                                                                                                                          TAGCAGAACTTCAGAGGGGAGCAGAGAGGCTCAGCTATCCACTGCTTGACACTGACCC 205367
                                                                                                                                                                                                                                                                                                                                                                   CAGCAAAACTTCGAAGCGAGCAGAGGGGTTCAGCTATCCACCGCTGCTTGACTCTGACC-
                                                                                                                                                                                                                                                                                                                                                                                                                    CCTCGGAGCTTTTCTACGACTTCCAGACGCAATTTACTCCAGGCGAGGGCGCCTGCAGTT
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                                                                                                                                                                                                                                                                                       ----ACCCGCAGCTCTCTGTTCTTTTGAGCCCGGAGTA
                                                                           CATTTTTTCCCAACCTCAGGATGGCGCCTCATCCCTTGGATGCGCCCACCATCCAAGTGT
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49898
79379
79479
132596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="UNK"
/clone="RP23-459M2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_name:Contig33"
27419. .49797
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132696. .215050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_name:Contig34"
49898 . 79378
/note="assembly_name:Contig35"
79479 . .132595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_name:Contig32"
16690. .27318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_name:Contig31"
4328. .16589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_name:Contig37"
52513 c 52885 g 53012 t
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4997: contig of 22379 bp in 16
49897: gap of unknown length
79378: contig of 29481 bp in 16
79478: gap of unknown length
132595: contig of 53117 bp in 16
132695: gap of unknown length
215050: contig of 82355 bp in 16
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Pred. No. 2.8e-212;
0; Mismatches 178;
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AC109783 138070 bp
Mus musculus clone RP23-121F10,
unordered pieces.
                                                                                                                                                           GAGTGACCTAATCCAGTGT 1460
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Direct Submission
Submitted (07-FEB-2002) Lita Annenberg Hazen Genome Sequencing
Submitted (07-FEB-2002) Lita Annenberg Hazen Genome Sequencing
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McCombie, W.R., Baker, J.P., Balija, V., Dedhia, N.N., de la Bastide, M., Katzenberger, F., Kuit, K., King, L., Kirchoff, K.A., Miller, B., Muller, S., Nascimento, L.U., O'Shaughnessy, A.L., Preston, R.R., Santos, L., Spiegel, L.A., Palmer, L., Yang, C. and Tutarorn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.cshl.org/genseq
Contact: mccombie@cshl.org
------Project Information
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Harbor, NY 11724, USA
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17874: gap of unknown length
30356: contig of 12482 bp in length
30444: gap of unknown length
42306: contig of 11862 bp in length
42398: contig of 11862 bp in length
53586: gap of unknown length
53686: gap of unknown length
64433: gap of unknown length
64443: gap of unknown length
74016: contig of 10669 bp in length
74016: gap of unknown length
74016: gap of unknown length
83366: contig of 9737 bp in length
83366: contig of 9822 bp in length
83365: contig of 8901 bp in length
92453: gap of unknown length
92455: contig of 8890 bp in length
100821: contig of 8378 bp in length
100821: contig of 6820 bp in length
107529: contig of 6820 bp in length
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107617: gap of unknown length
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Matches 1263; Conservative
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                 TGCACAACCTTAACTCCGCGCTGGATGCGCTGCGCGGTGTCCTGCCCCACCTTCCCCGGATG
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/db_xref="taxon:10090"
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                                    Diabetes (2001) In press

2 (bases 1 to 1861)

Schwitzgebel V. and German, M.

Direct Submission
Submitted (26-MAR-2001) Hormone Research Institute, University
California San Francisco, 513 Parnassus Ave, HSW1090, San
Francisco, CA 94145-0534, USA
                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 1861)
                                                                                                                                                                                                                                                               AF364300 1861
Mus musculus neurogenin 3 ger
AF364300.1 GI:13937128
                                                                                                                                     Regulation of the pancreatic
                                                                                                                                                   and
                                                                                                                                                                                                                          Mus
                                                                                                                                                                Lee, J., Smith, S.,
                                                                                                                                                                                                                                     Mus musculus
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               Location/Qualifiers
1. .1861
/organism="Mus musculus"
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ACCGCATGCACAACCTTAACTCCGCGCTGGATGCGCTGCGCGGTGTCCTGCCCACCTTCC
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                                           AGTTGGCACTGAGCAGCAGCGACGAAGCCGGCGCAAGAAGGCCCAACGACCGGGAGCGCCA
                                                                                GCCGAGGGACCTCGAGGAAGCTCCGCGCCCCGACGCGGAGGGCGCAACAGGCCCAAGAGCG
                                                                                               GCCGAGGGACATCGAGGAAGCTCCGTGCGCGGCGGCGGAGGGCGCAACAGGCCCAAGAGCG
                                                                                                                                       CCACCCCACCTAGCCCCACTCTCATACCTAGGGACTGCTCCGAAGCAGAAGTGGGTGACT
                                                                                                                                                                                              CCCCAGAGACAACAACCTTTTCCCGGAGCCTCGGACCACGAAGTGCTCAGTTCCAATT
                                                                                                                                                                                                              CCCAAGAGACCCAGCAACCCTTTCCCGGAGCCTCGGACCACGAAGTGCTCAGTTCCAATT
                                                                                                                                                                                                                                                  CATTTTTTCCCAACCGCAGGATGGCGCCTCATCCCTTGGATGCGCTCACCATCCAAGTGT
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                           AGTTGGCACTCAGCAAACAGCGAAGAAGCCGGCGCAAGAAGGCCAATGATCGGGAGCGCA
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/product="neurogenin 3"
/protein id="neurogenin 3"
/protein id="AAK50058.1"
/db_xref="GI:13937129"
/translation="MAPHPLDALTIQUSPETQOPFPGASDHEVLSSNSTPPSPTLIPR
DCSEARYGDCGTSRKLAARRGGRNRPKSELALSKORRSRRKKANDRERNRMININSA
LDALRGVLPTFPDDAKLTKIETLRFAHNYIWALTQTLRIADHSFYGPEPPVPCGELGS
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560 c 537 g 367 t
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1093. .1737
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/db_xref="taxon:10090"
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86.2%;
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Pred. No. 1.7e-191;
0; Mismatches 129;
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REFERENCE
AUTHORS
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ORGANISM
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                                Direct Submission
Direct Submission
Submitted (04-NOV-1996) G.J. Gradwohl,
Submitted (04-NOV-1996) G.J. Gradwohl,
CNRS-INSERM-Universite Louis Pasteur, /
                                                                                                                                           Jacquemin, P., Durviaux, S.M., Jensen, J., Godfraind, C., Gradwohl, G. Guillemot, F., Madsen, O.D., Carmeliet, P., Dewerchin, M., Collen, D., Rousseau, G.G. and Lemaigre, F.P.
Transcription factor hepatocyte nuclear factor 6 regulates pancreatic endocrine cell differentiation and controls expression of the proendocrine gene ngn3
                                                                                                                                                                                                                                                                                         Cau,
                                                                                                                                                                                                                                                                                                                                                bHLH; mammalian atonal homolog 4B; Mus musculus (house mouse)
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M.musculus MATH4B
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                        Revised
                                                                                    Gradwohl,G.J.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                      Mus musculus
Lemaigre, F.P.
                                                                                                                                                                                                                                                     Development 124 (8),
                                                                                                                                                                                                                                                                progenitors
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Local Similarity hes 997; Conserv
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Submitted (01-AUG-2000) Lemaigre F.P., Hormone and Metabol
Submitted (Unit, Louvain University Medical School, Avenue H
Research Unit, Louvain 1200, BELGIUM
75, box 7529, Brussels 1200, BELGIUM
On Oct 31, 2000 this sequence version replaced gi:1666087.
Location/Qualifiers
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                          Patent: WO 02086107-A 7 31-OCT-2002;
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(DE); INSTITUT FUER PFLANZENGENETIK UND KULTURPFLANZENFORSCHUNG
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              Location/Qualifiers
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CTGGTGTTCTCAGACTTCTTGTGAAGGGCCCAAACAGGCCCTGGGCGGTGGGCGCTGGCA 1139
                                                      TTGGAGGAGTTCCCTGGCCTGCAGGTGCCCAGCTCCCCATCCTGTCTGCTCCCGGGCACC
                                                                                                         GACTGGGGCTCTATCTACTCCCCAGTTTCCCAAGCTGGTAGCCTGAGCCCCACAGCCTCA
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DCSEABYGDCRGTSRKLRARRGGRNRPKSELALSKQRRSRRKANDRERNRMHNLNSA
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PGGGSNGDWGSIYSPVSQAGNLSPTASLEEFPGDQVPSSPSYLLPGALVFSDFL"
3 274 c 250 g 155 t
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
160. .804
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/db_xref="GI:29499590"
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Sommer, L., Ma, Q. and Anderson, D. J.

Sommer, L., Ma, Q. and Anderson and Anderson are perception factors; are putative mammalian neuronal determination genes that reveal progenitor cell heterogeneity in the developing CNS and PN (cell. Neurosci. 8 (4), 221-241 (1996)
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/function="bHLH
/note="NGN3"
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PGGGSNGDWGSIYSPVSQAGNLSPTASLEEFPGLQVPSSPSYLLPGALVFSDFL"
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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2 (bases 1 to 5340)
Lin,J: and German,M.
Direct Submission
Submitted (15-FEB-2000) Hormone Research Institute, Universi
California San Francisco, 513 Parnassus Ave., San Francisco,
94143-0534, USA
                                                                                                                                                Mammalia, Eutheria, Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 5340)

del Bosque-Plata, L., Lin, J., Horikawa, Y., Schwarz, P.E., Cox, N.J.

Iwasaki, N., Ogata, M., Iwamoto, Y., German, M.S. and Bell, G.I.

Mutations in the coding region of the neurogenin 3 gene (NEUROG are not a common cause of maturity-onset diabetes of the young
                                                                                                                         Japanese subjects
Diabetes 50 (3),
                                                                                                                                                                                                                                                                  Homo sapiens
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AF234829
                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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cancisco, CA
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AGTTGGCACTGAG 691 AGTTGGCACTGAG 3254	2 GAGGAAGCTCCGTGCGCGCGCGCGGAGGGCCCAACAGGCCCCAAGAGCGAGTTGGCACTGAG	Oy 63:
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CCACCCCACCTAG 571		ω
CCCAAGAGACCCA 511		Qy 45 Db 301
CATTTTTTCCCAA 451	5 GACCTCTAAGTCAGAGACTGTCACACCCCCCTTCCATTTTTTCCCAA	Qy 405 Db 2955
TCCCGCGTGGAGT 404	S GGAAC-CTCCAAAGGGTAGAAGAGGGGAGTGGGTGGGCGTACTCTAGTCCCGCGTGGAGT	Qy 346 Db 2895
TAGGTAACATTTA 345	S TGACTCTGACCACCCGCAGCTCTCTGTTCTTTTGAGCCCGGAGTAACTAGGTAACATTTA	Qy 286 Db 2835
ATCCACCGCTGCT 285	CAAAACTTCGAAGCGAGCAGAGGGGTTCAGCTATCCACCGCTGCT	Qy 241 Db 2775
GCCTGCAGCTCAG 240 GCCTGCAGCTCAG 2774	GAAGCTTCTTTGCTGCCTCCAGACGCAATTTACT-CCAGGCGAGGGGGCCTGCAGCTCAG	Qy 182 Db 2715
CGAGGACCCCCTC 181	CCCTCTGGGTCTCACCACTGC	Qy 140 Db 2655
GCAGCTCAGAAGT 139 GCTGCTCAGGAAA 2654	O CCTGGTCCGGGCAGAGCAGATAAAGCGTGCCAGGGGACACACGATTAGCAGCTCAGAAGT	Qy 80 Db 2595
CGGCAGGCACGCT 79 GGGCAGGCACGCT 2594	GTCCCTGGGCCCCCGTTGCTGATTGGCCCCGTGGCAGGCA	Qy 20 Db 2535
5340; 48; Gaps 5;	35.4%; Score 517.4; DB 9; Length Similarity 67.4%; Pred. No. 1.3e-105; conservative 0; Mismatches 351; Indels	Query Match Best Local : Matches 82
DEVTCPTSAPPSPTRTRG RKKANDREENRMHNIASA DHSLYALEPPAPHCGELG ACLSPGSLAFSDFL"	/product="neurogenin 3" /product="neurogenin 3" /product=in_id="AAK15022.1" /db_xref="GI:13183003" /translation="MTPQPSGAPTVQVTRETERSFPRASEDEVTCPTSAPPSPTRTRG /translation="MTPQPSGAPTVQVTRETERSFPRASEDEVTCPTSAPPSPTRTRG /translation="MTPQPSGAPTVQVTRETERSFRASKQRRSRKKANDREENRMHNINSA NCAEAEEGCCRGAPRKLRARRGGRSRPKSELALSKQRRSRKKANDREENRMHNINSA LDALRGVLPTFPDDAKLTKIETLRFAHNYIWALTQTLRIADHSLYALEPPAPHCGELG SPGGSPGUMGSLYSPVSQAGSLSPAASLEERPGLLGATSSACLSPGSLAFSDFL" 1215 a 1500 c 1514 g 1111 t	BASE COUNT
	/product="neurogenin 3" 30223666 /codon start=1	CDS
	= 27 0	mRNA .
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                                                  AAGGTAGTGGAGGCACTCGAGCATC 1196
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ÀGGGTGGCCGÀCGGCGGCGGCCCTC 3759
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REFERENCE AUTHORS SOURCE ORGANISM ACCESSION VERSION KEYWORDS RESULT 12 AL450311/c LOCUS DEFINITION AL450311 165110 bp DNA linear PRI 12-JUL-2001 Human DNA sequence from clone RP11-343U3 on chromosome 10, complete AL450311.11 HTG. AL450311 sequence

TITLE JOURNAL Submitted (12-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone Homo sapiens Howden, P. Direct Submission Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; Homo sapiens (human) (bases 1 to 165110) Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

COMMENT

requests: clonerequest@sanger.ac.uk
On Jul 8, 2001 this sequence version replaced gi:14575291.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred*quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; Sw:,
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is the entire insert of clone RP11-343J3 The true left end of clone RP11-242G2O is at 139955 in this sequence. The true right end of clone RP11-404C6 is at 6588 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VECTOR: pBACe3.
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                                                                                                                                                              /note="MIR repeat:
19169. .19400
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="AluSq repeat: matches 243. .299 of consensus"
14843. .14943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            )662. .6438
/note="L1MEc repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  319. .4494
'note="Alusx repeat: matches 118. .293 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :144. .4270
|/note="AluSx repeat: matches 1. .134 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="26 copies 2 mer gt 98% conserved"
2960. .3272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="THEIC repeat: matches 2. .142 of consensus"
151. .293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="RP11-343J3"
/clone_lib="RPCI-11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="10"
                     19969. .20010
/note="21 copies 2
                                                                                                                                                                                                                                                                                                                                               note="MIR repeat: matches 60. .140 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                         note="MIR repeat: matches 3. .213 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="AluSg repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note≃"MIR repeat: matches 2. .148 of consensus"
                                                                                                     'note="L1MC5 repeat:
                                                                                                                                                                                                      note="L1MC4 repeat: matches 7617. .7977 of consensus" 8117. .18345
                                                                                                                                                                                                                                                                                                                                                                                                                                 note="MER86 repeat: matches 9. .109 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="MLT1C repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="20 copies 2 mer tc 95% conserved"
2479. .12608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="AluSx repeat: matches 1. .294 of 1600. .11639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="MIR repeat: matches 65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="L1MEc repeat: matches 1168. .2367 of consensus"
                                                             note="MIR repeat: matches 48.
                                                                                    9642. .19716
                                                                                                                                             note="MIR repeat: matches 5. .239 of consensus"
                                                                                                                                                                                                                                                                                                                              6928. .16993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4372 .14576
note="AluSg repeat: matches 1 .301 of consensus"
                                                                                                                                                                                                                                                                   note="MER81 repeat:
                                                                                                                                                                                                                                                                                          note="33 copies 2 mer gg 66% conserved"
7476. .17569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="65 copies 2 mer at 90% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="MIR
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                     mer tg 100% conserved"
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            /note="MER58A repeat: matches 37.
45798. .45909
/note="LTR41 repeat: matches of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="41 copies 2 mer gt
20738. .20773
                                                                                                                   /note="L2 repeat: matches 1916. .2416 of consensus" 42388. .42698 /note="L2 repeat: matches 1448. .1779 of consensus" 44193. .44579 /note="THEIC repeat: matches 1. .371 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                   36551. .36604

'note="27 copies 2 mer ac 94% conserved"

37585. .38254

'note="LiPA15 repeat: matches 5480. .6157 of consensus"

38265. .38561

'note="Alusx repeat: matches 1. .300 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="AluJb repeat: matches 1.
23838. .24137
/note="L2 repeat: matches 1754.
                                                                                                       44600. .44956
                                                                                                                                                                                                                                                                                                                                                    39214. .39423
/note="MIR repeat: matches 3.
39489. .39801
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3533. .23837
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                                                                                     'note="LTR16A
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note="MIR repeat: matches 46.
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                                                                                                                                                                                                                1506. .41944
                                                                                                                                                                                                                              1296. .41460
note="L2 repeat:
                                                                                                                                                                                                                                                               1057. .41290
note="MIR repeat: matches 8. .240 of consensus"
                                                                                                                                                                                                                                                                                                 note="MIR repeat: matches 1.
                                                                                                                                                                                                                                                                                                                   note="AluSx repeat: matches 1. 0050. .40189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="43 copies 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1618. .31876
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AGCAAGCAGCGACGAAGCCGGCGCAAGAAGGCCAACGACCGGGAGCGCAACCGCATGCAC
                                                                                                                                                GAGCGGTCCTTCCCCAGAGCCTCGGAAGACGAAGTGACCTGCCCCACGTCCGCCCCGCCC
                                                                                                                                                                   CAGCAACCCTTTCCCGGAGCCTCGGACCACGAAGTGCTCAGTTCCAATTCCACCCCACCT
                                                                                                                                                                                                    CGCCGTAGGATGACGCCTCAACCCTCGGGTGCGCCCACTGTCCAAGTGACCCCGTGAGACG
                                                                                                                                                                                                                        AACCTCAGGATGGCGCCTCATCCCTTGGATGCGCCACCATCCAAGTGTCCCAAGAGACCC
                                                                                                                                                                                                                                                                                                           TGACTCTGACCACCCGCAGCTCTCTTGTTTTTTGAGCCCGGAGTAACTAGGTAACATTTA
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                                                          TCGAGGAAGCTCCGTGCGCGGCGCGAGAGGGCCCAACAGGCCCAAGAGCGAGTTGGCACTG
                                                                                                             AGCCCCACTCTCGTACCGAGGGACTGCTCCGAAGCAGAAGCAGGTGACTGCCGAGGGACA
                                                                                                                                                                                                                                                      AGCCTCGGAATCGCGGACTGCGCCCAGTGACGGACTCAAACTTACCCTTCCCTCTGACCC
                                                                                                                                                                                                                                                                                                                                    GGAACCTCCAAAGGGTAGAAGAGGGGAGTGGGTGGGCGTACT---
                                                                                                                                                                                                                                                                                                                                                                TATTCTTTTGCGCCGGTAGAAAGGTAATATTTGGAGGCCTCCGAGGGACGGGCAGGGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAAACTTCGAAGCGAGCAG-----
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                                                                                            AGCCCCACTCGCACACGGGGAACTGCGCAGAGGCGGAAGAGGGGAGGCTGCCGAGGGGCC
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/note="MLT1A1 repeat:
55237. .55700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="AluSx repeat: 52222. .52519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="23 copies 2 mer gt 50684..50969 /note="AluSq repeat: match 50980..51291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54648. .54862
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54261. .54432
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54065. .54260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="FAM repeat: matches 2. .167
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                                                                                                                                                                                                                                                                                                                                                                                      AC021954.3 GI:7417809
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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30094 AGCAAGCAGCGACGGAGTCGGCGAAAGAAGGCCCAACGACCGCGAGCGCAATCGAATGCAC
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AGAGGGTGGCCGACGGCGGCGCCCTC 29588
                                                             GGAAGGTAGTGGAGGCACTCGAGCATC
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                                                                                                                                    CAAACAGGCCCTGGGCGGTGGGCGCTGGCAGAAAGGGAAGGGAAGTCAGAGCTGTCTGAAAT 1169
                                                                                                                                                                                                                                                                         ACCTTTTCCGCCTGCTTGAGCCCAGGCAGTCTGGCTTTCTCAGATTTTCTGTGAAAAGGAC
                                                                                                                                                                                                                                                                                                                                             AGCTCCCCATCCTGTCTGCTCCCGGGCACCCTGGTGTTCTCAGACTTCTTGTGAAGGGCC 1109
                                                                                                                                                                                                                                                                                                                                                                                                                  CAGGCTGGCAGCCTGAGTCCCGCCGCGTCGCTGGAGGAGCGACCCGGGCTGCTGGGGGCCC
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Eukaryota; Metazoa; Chordata; Craniata; Verteb Mammalia; Eutheria; Primates; Catarrhini; Homi 1 (bases 1 to 173341)
Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 10, clone RP11-57E12 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

HTG 24-A WORKING

Birren, B., Linton, I., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Edguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Ferestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, R., Lieu, C., Liu, G., Locke, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Timrer, A. and Zody, M., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Submitted (22-JAN-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 173341) Direct Submission Zimmer, A. and Zody, M. for Genome

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COMMENT
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G.,
Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,
Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Center clone name: 57_E l2
Sequencing vector: M13; M77815; 100% of reads
Center vector: M13; M77815; 100% of reads
Center vector: M13; M77815; 100% of reads
Center vector: M13; M77815; 100% of reads
Assembly program: Phrap; version 0.960731
Center vector: M13; 16190 bases at least Q40
Censensus quality: 166837 bases at least Q30
Censensus quality: 168935 bases at least Q20
Insert size: 171041; sum-of-centiss
Center vector ve
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18932. .23526
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/clone lib="RPCI-11 Human Male BAC"
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/mol_type="genomic DNA"
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89547. .96459
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81427. .89446
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128991. .147290
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96560. .106498
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147391. .173341
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Submitted (16-MAR-1999)
de la Pitie Salpetriere,
PARIS, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens gene for neurogenin 3.
AJ133776
AJ133776.1 GI:5123782
bHLH transcription factor; neurogenesis; neurogenin Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 1330) Ravassard, P.
                                                                                                                                                                                                                                                                                                                                     Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                                                                               The human neurogenin 3 homolog maps to chromosome 10q21.3 and its expression pattern is identical to that of its murine counterparts
                                                                                                                                                                                                                                                                                                                                                                                                   Mallet,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                Ravassard, P., Icard-Liepkalns, C., Wiard, L., Julien, J.P. and
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                                                                     GTTCTCAGACTTCTTGTGAAGGGCCCAAACAGGCCCTGGGCGGTGGGCGCTGGCAGAAAG
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 GGAGAGGGAGGGGGGGGGGGCCGTAGAGGGTGGCCGACGGCGGCGGCCCTC
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CE 2 (bases 1 to 170896)

RS Birren, B., Linton, L., Musbaum, C., Lander, E., Allen, N., Anderson, M.,

RS Birren, B., Linton, L., Musbaum, C., Lander, E., Boukhgalter, B.,

Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,

Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,

Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,

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Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Klein, J.,

Howland, C.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,

Heboczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,

McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,

Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,

Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,

Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,

Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,

Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (29-SEP-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 28, 2000 this sequence version replaced gi:6479051.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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Birren,B., Linton,L., Nusbaum,
Homo sapiens, Clone RP11-6P16
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Mammalia; Eutheria; Primates;
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Homo sapiens clone RP11-6P16, WORKING DRAFT SEQUENCE,
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* consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: L2916
Center clone name: 6 P 16
Center clone name: 6 P 16
Sequencing vector: M3; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 114103 bases at least Q40
Consensus quality: 141555 bases at least Q20
Consensus quality: 158230 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                 Insert size: 154000; agarose-fp Insert size: 16889; sum-of-contigs Ouality coverage: 3.6 in Q20 bases; Quality coverage: 3.3 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: sequence submissions@genome.wi.mit.edu
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9: contig of 10146 bp in levil gap of 100 bp
13: contig of 10674 bp in levil gap of 100 bp
63: contig of 12330 bp in levil gap of 100 bp
19: contig of 11056 bp in live gap of 100 bp
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TGGCCGÁCGGCGGCGCCCTC
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Pred. No. is the number of results predicted by chance to I score greater than or equal to the score of the result being and is derived by analysis of the total score distribution. chance to have a result being printed,

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8	ი თ	ω a.	2	1	Result No.	
652 652	682.4 682.4	899.6 819.8	900.6	1458.4	Score	
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19 21	25 25	24 22	21	19		
AAV27050 AAZ51981	AAF27266 ABV75970	AAD46872 AAF27254	AAC61090	AAV42512	ID	SUMMARIES
Mouse neurogenin 3 Murine neurogenin-	Mouse neurogenin 3 Mouse transcriptio	Murine neurogenin Mouse atonal homol	Murine neurogenin	cDNA encoding a no	Description	

TS	ALIGNMENTS						
Mouse neurogenic d	AAT74893	18	1951	6.4	93.2	4 5	
Human NeuroD2 gene	AAA62681	21	1550		96	44	
Human bHLH family	ABS56389	25	1535		96	43	
DNA encoding human	AAV42931	19	1535		96	42	
Human neurogenic d	AAT74890	18	1535		96	41	
	ABQ16591	24	778	7.3	106.6	40	
Oligonucleotide fo	ABQ16590	24	778		٥,	39	Ω
	AAZ51979	21	1277		9	38	
	AAV27048	19	1277		9	37	
	AAZ51978	21	1312	٠	115.6	36	
	AAV27047	19	1312	•	57	ω 5	
. Chicken atonal hom	AAF27263	22	1074	•		34	
Human neurogenin 2	AAD46890	24	6123	٠	•	33	
Chicken atonal hom	AAF27264	22	790	•		32	
	AAF27273	22	1412	٠		31	
	AAF27255	22	1412	•	139.8	30	
Mouse neurogenin 2	AAF27269	22	1385		•	29	
	AAZ51980	21	1385	9.6	•	28	
neurogenin	AAV27049	19	1385	•	•	27	
Mouse neurogenic d	AAT74894	18	1333	•		26	
Mouse bHLH family	ABS56396	25	1332	•	•	25	
DNA encoding murin	AAV42938	19	1332	•	•	24	
Murine neurogenin-	AAZ51977	21	738	•	•	23	
se neurogenin	AAV27046	19	738	•	•	22	
Rat neurogenin-1 (AAZ51976	21	1527	•	•	21	
	AAV27045	19	1527	9.9	٠	20	
Human neurogenin 1	AAD46888	24	1665	10.1	147.6	19	
Human bHLH family	ABS56390	25	1268	•	•	18	
DNA encoding human	AAV42932	19	1268	10.1	147.6	17	
Human neurogenic d	AAT74891	18	1268	•	•	16	
Human neurogenin 1	AAD46889	24	714	•	147.6	15	
	ABQ49525	24	592	•	٧	14	ი
Oligonucleotide fo	ABQ49524	24	592	w	.~	13	
	ABQ49523	24	592	15.7	9	12	
	ABQ49522	24	592	5	9.	11	a
neurogenin	468	24	5340	35.4	517.4	10	
Human neurogenin 3	AAC61089	21	5340	35.4	517.4	9	

RESULT 1 AAV42512 ID AAV XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Basic helix-loop-helix polypeptide and related nucleic acid transcriptional activity, for targeting expression of genes central nervous system and treatment of nervous disease
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hes 1459;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The human neurogenin 3 Ngn3 DNA sequence AAC61089 encodes the Ngn3 protein AAY85617. The Ngn3 gene is located at chromosome position 10q22.1-22. The invention relates to the human Ngn3 nucleotide and protein sequences, and includes an antibody recognising the Ngn3 protein. Also included in the invention is a method for identifying an islet cell precursor, the method involves analysing a cell for the expression of the Ngn3 gene product, where detection of the product is indicative of an islet cell precursor. The Ngn3 DNA sequence is useful as a diagnostic reagent for detecting (in a subject) a predisposition to a defect in pancreatic islet cell function or formation associated with a defect in Ngn3 activity. The Ngn3 protein is useful for identifying beta-cell precursor cells expressing Ngn3, and to alter cellular differentiation in culture in vivo to produce new beta-cells to treat patients with diabetes mellitus. The present sequence represents the murine Ngn3 genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human neurogenin 3 polypeptides and polynucleotides encoding them, useful for diagnosis, prevention and treatment of diabetes mellitus and to identify individuals at risk of diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1861
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   TATCCACTGCTTGTCACTGACTGACCTGCTCTATTCTTTTGAGTCGGGAG-
                                                                                                                                           CAGCAAAACTTCGAAGCGAGCAGAGGGGTTCAGCTATCCACCGCTGCTTGACTCTGACC-
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                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method for producing a mammalian islet cell. The method comprising introducing into a mammalian cell a nucleic acid molecule encoding an islet transcription factor for expression of the islet transcription factor in the cell and for production of islet cell phenotype in the cell. The islet transcription factor is neuroendocrine basic helix-loop-helix (bHLH) transcription factor. The method is useful for treating type 2 diabetes mellitus and for replacing beta cells lost to autoimmune destruction in individuals with type 1 diabetes. The method is useful for cell in cell therapy. The present sequence is murine neurogenin 3 means force.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding neuroendocrine basic helix-loop-helix transcription
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P-PSDB; AAE29278.
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Pred. No. 9.2e-235;
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                                                                                                                                                                                                                                                                                                                                    The invention relates to the use of atomal-associated nucleic acid or CC amino acid sequence, or any of its homologues or orthologues as CC therapeutic agents for the treatment of deafness, partial hearing loss, CC vestibular effects due to damage or loss of inner hair cells, CC vestibular effects due to damage or loss of inner hair cells, CC encompasses methods of screening for compounds which affect the CC encompasses methods of screening for compounds which affect the CC expression of an atomal-associated nucleic acid sequence, in an animal, CC and a transgenic animal in which an allele of a native atomal-associated CC gene is replaced by a heterologous nucleic acid sequence, thus CC inactivating the atomal-associated allele. The nucleic acids or proteins CC may be used in a method of treating an animal for hearing impairment, CC disease related to loss of a functional atomal-associated nucleic acid or protein. They may particularly be used to treat an animal with a CC deficiency in cerebellar granule neurons or their precursors, and may CC also be used in promoting mechanoreceptive cell growth and generating CC acid sequence referred to in the invention.

CC Note: The present sequence represents an atomal-associated nucleic acid sequence referred to in the invention.
                                                                                                                                                                                                                                      Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Atonal; homologue; orthologue; atonal-associated protein; deafness; hearing impairment; vestibular effect; balance disorder; osteoarthritis; cellular proliferation; cerebellar granule neuron; gene therapy; mechanoreceptive cell growth; auditory; osteopathic; cytostatic;
                                                                                                                                                                                                                                                                                               Sequence
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19-JAN-2000;
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                                                                                                                                                                                                                                                                                                         The invention relates to the use of atomal-associated nucleic acid or CC amino acid sequence, or any of its homologues or orthologues as CC therapeutic agents for the treatment of deafness, partial hearing loss, CC vestibular effects due to damage or loss of inner hair cells, CC osteoarthritis and abnormal cell proliferation. The invention also CC encompasses methods of screening for compounds which affect the CC expression of an atomal-associated nucleic acid sequence in an animal, CC and a transgenic animal in which an allele of a native atomal-associated gene is replaced by a heterologous nucleic acid sequence, thus CC inactivating the atomal-associated allele. The nucleic acids or proteins CC may be used in a method of treating an animal for hearing impairment, CC disease related to loss of a functional atomal-associated nucleic acid or CC disease related to loss of a functional atomal-associated nucleic acid or CC disease related to loss of a functional atomal-associated nucleic acid or CC disease related to loss of a functional atomal-associated nucleic acid sequence referred to in the invention.

CC also be used in promoting mechanoreceptive cell growth and generating CC hair cells. The present sequence represents an atomal-associated nucleic acid sequence referred to in the invention.
                                                                                                                                                                                                                                     Best Local Sim
Matches 771;
                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Therapeutic use of atonal-associated nucleic acids or amino any of its homologs or orthologs, for the treatment of e.g. osteoarthritis and abnormal cell proliferation -
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GCGCCCACCATCCAAGTGTCCCAAGAGACCCAGCAACCCTTTCCCCGGAGCCTCGGACCAC 539
                                                                 CTG--TCACACCCCCTTCCATTTTTTCCCAACCTCAGGATGGCGCCTCATCCCTTGGAT
                                                                                                                                                                                          TTCTTTTGAGCCCGGAGTAACTAGGTAACATTTAGGAACCTCCAAAGGGTAGAAGAGGGG
                                                                                                  CGCGCGGGGTGTGTGGGGGGATACTCTGGTCCCCCGTGCAGTGACCTCTAAGTCAGAGG
                                                                                                                                                                   TTCTTTTGAGTCGGGAG-AACTAGGTAACAATTCGGAAACTCCAAAGGGTGGATGAGGGG
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                                                                                                                                                                                        Mouse transcription factor neurogenin
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                                                                                                        Mus musculus
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a gene which is required for the specification of the early endocrine which is required for the specification of the early endocrine precursor in the pancreatic epithelium and which is down-regulated once endocrine differentiation begins. The invention provides a claimed method for differentiating stem cells (especially embryonic, adult or somatic stem cells and primordial germ cells) into insulin-producing cells. This involves culturing stem cells in a suitable medium and activating at least one gene involved in beta-cell differentiation. Preferred genes including Pdx1, Pax4, Pax6 and ngn3 (see ABVT5967-70). Gene activation comprises the cells end ngn3 (see ABVT5967-70). Gene activation comprises the system, or the delivery of a protein product of the gene into stem cells. The insulin-producing cells can be transplanted into animals or human for treatment of pancreatic diseases, metabolic syndrome and metabolic disorders with impaired glucose levels such as diabetes, hyperglycaemia and impaired glucose tolerance (claimed). The cells can also be used to identify compounds which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (claimed). The cells can also be used to recommend or glucose stimulate beta-cell differentiation, insulin secretion or glucose responsiveness. Differentiated beta-cells can be used to study the toxic and other effects of exogenous compounds on beta-cell function. In an example from the invention, Pax6 cDNA was inserted function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is that of cDNA encoding the murine basic helix-loop-helix transcription factor neurogenin 3 a gene which is required for the specification of the ea
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12-NOV-1996;
19-DEC-1996;
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the proteins are usefu
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CTGGTGTTCTCAGACTTCTTGTGA 1103
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                                                                        TTGGAGGAATTCCCTGGCCTGCAGGTGCCCAGCTCCCATCCTATCTGCTCCCGGGAGCA
                                                                                                   TTGGAGGAGTTCCCTGGCCTGCAGGTGCCCAGCTCCCCATCCTGTCTGCTCCCGGGCACC
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90.9%;
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Pred. No. 1.9e-167;
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                                                                                                                                                                                                                                                                                                                                                               Neurogenin-3; NGN-3; non-neuronal cell; NNC; neurogenesis; Phox2a protein; neuronal subtype-specific marker; growth facto neural differentiation; transplantation; neuronal dysfunction;
                                                                                                                                                                                                                                                                                                                                                                                           Murine neurogenin-3 (NGN3) nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                          04-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ51981;
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Inducing non-neuronal cells to differentiate into neurons and for non-neuronal cells to express a neuronal subtype-specific marker, comprising contacting the non-neuronal cells with a vector containing neurogenin nucleic acid -

P-PSDB; AAY70570.

2000-256250/22

<u>5</u>

14-AUG-1998;

98US-0096630 99WO-US18525

(CALY) CALIFORNIA INST OF TECHNOLOGY.

Claim 1; Fig 1J; 76pp; English.

The patent discloses a method for inducing non-neuronal cells (NNC) to differentiate into neurons and for NNCs to express a neuronal subtype CC differentiate into neurons and for NNCs to express a neuronal subtype CC especific marker. Transformed host cells are used as sources of neuronal CC and other growth factors; in culture for screening compounds that CC modulate neural differentiation or as sources of recombinantly produced CC neurogenins and phox2a proteins for use in transplantation. The cells CC also have a variety of in vivo uses, e.g. for transplantation at sites of CC neuronal dysfunction e.g. patients with hearing or vision loss due to CC optical or auditory nerve damage, brain or spinal cord injuries, and CC neurodegenerative disorders e.g. Alzheimer's disease. The present CC sequence encodes murine neurogenin-3 (NGN-3), a transcription factor. CC NNCs differentiate into neurons through the recombinant expression of a CC transcription factor that induces a core program of neurogenesis. Forced CC expression of murine NGN3 can ellcit expression of at least some neuronal vy

Sequence 804 BP; 171 A; 263 Ç 225 G; 145 T; 0 other;

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Query Match
Best Local S
Matches 731
        Similarity
      44.7%;
90.9%;
Score 652; DB Pred. No. 1.9e 0; Mismatches
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        .9e-167;
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TTCTTTTGAGCCCGGAGTAACTAGGTAACATTTAGGAACCTCCAAAGGGTAGAAGAGGGG

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                                                                                                                                    Neurogenin 3; Ngn3; chromosome 10q22.1-22.2; cellular differentiation; islet cell precursor identification; diabetes mellitus; human; ds.
                                                                                                                                                                                                       Human neurogenin 3
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Best Local Similarity
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DB; AAE29277.
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                                                                                                                                                                                                                                               TCCCTGCGGTCTCACCGCCCCCCCCCCAGAGAGAGAGCCTGACAGAGGCCTCGGACCCCATT
                                                                                                                                                                                                                                                                CCCTCTGGGTCTCACCACTGC-----
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  GACCTCTAAGTCAGAGACTG----
                           AGAGGGATCCTCTGACCCAGCGGGGGGCTGGGAGGATGGCTGTTTTTGTTTTTTCCCACCT
                                                      GGAAC-CTCCAAAGGGTAGAAGAGGGGAGTGGGTGGGCGTACTCTAGTCCCGCGTGGAGT
                                                                                                                                    CTGAACTTGGCGACCAGAAGCCCGCTGAGCTCCCCACGGCCCTCGCTGCTCATCGCTCTC
                                                                                                                                                              CAAAACTTCGAAGCGAGCAG----
                                                                                                                                                                                          CTCTCTTCTTTTCTCCTTTGGGGCTGGGGCAACTCCCAGGCGGGGGGCGCCTGCAGCTCAG
                                                                                                                                                                                                                                                                                                   CCTGGCCCGGGCGAAGCAGATAAAGCGTGCCAAGGGGCACACGACTTGCTGCTCAGGAAA
                                                                                TATTCTTTTGCGCCGGTAGAAAGGTAATATTTGGAGGCCTCCGAGGGACGGGCAGGGGAA
                                                                                                       TGACTCTGACCACCGCAGCTCTCTGTTCTTTTGAGCCCGGAGTAACTAGGTAACATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 87-88; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002WO-US11166
                                                                                                                                                                                                                                                                                                                                                                                                                                                             B₽;
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    -TCACACCCCCCTTCCATTTTTCCCAA
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AGGGGTTCAGCTATCCACCGCTGCT

285

2774 240 2714

2834

451

2954 404 2894 345 ACAGAGGCCGAGGACCCCCTC

181 2654 139 2594 79 IJ

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The invention relates to a method for producing a mammalian islet cell. The method comprising introducing into a mammalian cell a nucleic acid molecule encoding an islet transcription factor for expression of the islet transcription factor in the cell and for production of islet cell phenotype in the cell. The islet transcription factor is a neuroendocrine basic helix-loop-helix (bHLH) transcription factor. The method is useful for treating type 2 diabetes mellitus and for replacing beta cells lost to autoimmune destruction in individuals with type 1 diabetes. The method is useful in cell therapy. The present sequence is human neurogenin 3 (Ngn3) gene. Ngn3 gene is located on chromosome 10q22.1-22.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g a mammalian islet cell for treating diabetes mellitus s introducing into a mammalian cell a nucleic acid moleoneuroendocrine basic helix-loop-helix transcription fac
Score 517.4; DB 24;
Pred. No. 1.8e-130;
0; Mismatches 351;
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useful of

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ABQ49522/c
ID ABQ495
XX ABQ495
XX ABQ495
XX ABQ495
XX OBQ495
XX Oligon
XX Human;
XW drug;
XW drug;
XW drug;
XW drug;
XW Gastro;
XW SNP; co
                                                                    Human; cytosine methylation; 5"-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism, SNP; cell differentiation; ds.
                                                                                                                                                                                          Oligonucleotide for detecting
                                                                                                                                                                                                                                                                                                                                             ABQ49522 standard; DNA; 592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCTGGTAGCCTGAGCCCCACAGCCTCATTGGAGGAGTTCCCTGGCCTGCAGGTGCCCAG 1051
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sapiens

nucleotide polymorphism;

CCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAGATCGAGACCCTGCGCCTTCGCCCA 844

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic CC The amplicon is hybridised to two classes, each with at least one CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers CC and the degree of hybridisation to both classes is determined from the CC lasses of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide cystems etc., particularly by detecting mutations or single nucleotide cypes and for investigating cell differentiation. The method allows the CC methylation status of many C residues to be determined simultaneously.

CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 592 BP;
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05-SEP-2000; 2000DE-1044543.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the disclosure of the invention.
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 177
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                                                                        237
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                                                                                                                                                                                                                                                                                                                  CACCATCCAAGTGTCCCAAGAGACCCAGCAACCCTTTCCCGGAGCCTCGGACCACGAAGT
                        CGACCGGGAGCGCAACCGCATGCACAACCTTAACTCCGCGCTGGATGCGCTGCGCGGTGT 784
                                                                                                          CAGGCCCAAGAGCGAGTTGGCACTGAGCAAGCAGCGACGAAGCCCGGCGCAAGAAGCCCAA 724
                                                                                                                                              GARARARARARACTACCGARARACCCCCGARARARACTCCGARCACGACGCGARARARACGCAR
                                                                                                                                                                                 MACCTACCCACGTCCGCCCCGCCCAACCCCACTCGCACACGAAAAAACTACGCAAAAAC
                                                                                                                                                                                                                                                         GCTCAGTTCCAATTCCACCCCACCTAGCCCCACTCTCGTACCGAGGGACTGCTCCGAAGC
                                                                                                                                                                                                                                                                                               CACTATCCAAATAACCCGTAAAACGAAACGATCCTTCCCCAAAACCTCGAAAACGAAAT 358
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                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 229.6; DB Pred. No. 2e-52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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Gaps

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RESULT 12
ABQ49523
ID ABQ49
XX Oligc
XX Humar
XX Gast;
XX Gast;
XX Ol-6
PD Ol-6
XX Ol-6
CC Ol-7
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                                                                                                                                                                                           This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic CC The amplicon is hybridised to two classes, each with at least one CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers CC and the degree of hybridisation to both classes is determined from the CC lasses of oligomers, the degree of methylation is calculated. The method is used: (1) for diagnosis and/or prognosis of side effects of CC is used: (1) for diagnosis and/or prognosis of side effects of CC is used: (1) for diagnosis and/or prognosis of side effects of CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide collymorphisms (SNP's), and (ii) for differentiation. The method allows the CC methylation status of many C residues to be determined simultaneously.

CC AB013410-AB054121 represent genomic DNA sequences used to illustrate the method of colling the degree of cytosine methylation described in the invention.
Best Local Sin Matches 322;
                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      drug; side effect; cancer; central nei
gastrointestinal; respiratory system;
SNP; cell differentiation. An
                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Determining the degree of cytosine methylation for diagnosis and prognosis, comprises selective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-371829/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-SEP-2000;
05-SEP-2000;
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                                                                                                                      C; 59 G;
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Pred. No. 2e
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em; single nucleotide polymorphism;
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                                    2e-52;
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                                                            DB 24; Length 592;
                                                                                                                         0 other;
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Conservative

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Mismatches

Indels

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Gaps

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This invention describes a novel method for determining the degree methylation of a particular cytosine in a motif 5'-CpG-3', present

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                                                               Determining the degree of cytosine methylation in genomic for diagnosis and prognosis, comprises selective hybridiza amplicons from chemically treated DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide
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                                    Claim 12; 56pp + Sequence
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05-SEP-2000;
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                                                                                                                                             Piepenbrock C,
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2000DE-1044543.
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                                      Listing; 56pp; German
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hybridization
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RESULT 14
ABQ49525/c
ID ABQ495
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AC ABQ495
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DT 12-JUL
XX
COligon
XX
KW Human;
KW drug;
KW drug;
KW gastro
KW SNP; c
XX
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                 drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphi SNP; cell differentiation; ds.
                                                                    Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
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Pred. No. 3.1e
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CC genomic sample of DNA. The sample is treated chemically to convert CC CDNA that contains the target C is amplified to form a labeled amplicon. CC DNA that contains the target C is amplified to form a labeled amplicon. CC The amplicon is hybridisacton to both classes, each with at least one CC and the degree of hybridisaction to both classes is determined from the CC and the degree of hybridisaction to both classes is determined from the CC classes of oligomers, the degree of methylation is calculated. The method CC is used: (i) for diagnosis and/or prognosis of side effects of the rapeutic drugs and of a wide range of diseases, e.g. cancer, disorders CC of the central nervous, cardiovascular, gastrointestinal and respiratory contypes and for investigating cell differentiation. The method acceptable in the contypes and for investigating cell differentiation. The method allows the contypes and for investigating cell differentiation. The method allows the CC methylation status of many C residues to be determined simultaneously. CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the CC method for determining the degree of cytosine methylation described in CC the disclosure of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel method for determining methylation of a particular cytosine in a motif 5'-Cpg-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 12; 56pp + Sequence Listing; 56pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-SEP-2000;
05-SEP-2000;
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                                                                                                                                                                                                                                                                              CCCTTTCCCGGAGCCTCGGACCACGAAGTGCTCAGTTCCAATTCCACCCCACCTAGCCCC 575
                                                 TAGCGACGGAGTCGGCGAAAGAAGGTTAACGATCGCGAGCGTAATCGAATGTATAATTTT
                                                                         CAGCGACGAAGCCGGCGCAAGAAGGACCCAACGGACCGGAACCGCATGCACAACCTT
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AAGTTTCGGGTACGGCGGGGGACGTAGTCGGTTTAAGAGCGAGTTGGTATTGAGTAAG
                                                                                                                                                            AAGCTCCGTGCGCGGCGCGAGGGCGCAACAGGCCCAAGAGCGAGTTGGCACTGAGCAAG
                                                                                                                                                                                                   ATTCGTATACGGGGAATTGCGTAGAGGCGGAAGAGAGGTTGTCGAGGGGTTTCGAGG
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2000DE-1044543
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64.5%;
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AATTCGGTATTGGACGTTTTGCGCGCGGTGTTTTGTTTATTTTTTTAGACGACGCGAAGTTT

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Best Local Sim
Matches 195;
                                                                                                                                The invention relates to a method for producing a mammalian islet cell. The method comprising introducing into a mammalian cell a nucleic acid molecule encoding an islet transcription factor for expression of the islet transcription factor in the cell and for production of islet cell phenotype in the cell. The islet transcription factor is a neuroendocrine basic helix-loop-helix (bHLH) transcription factor. The method is useful for treating type 2 diabetes mellitus and for replacing beta cells lost to autroimmune destruction in individuals with type 1 diabetes. The method is useful in cell therapy. The present sequence is human neurogenin 1 (Ngn1) gene.
                                                                                                                                                                                                                                                                                     Disclosure; Page 94; 108pp; English.
                                                                                                                                                                                                                                                                                                              Producing a mammalian islet cell for treating diabetes mellitus comprises introducing into a mammalian cell a nucleic acid molecule encoding neuroendocrine basic helix-loop-helix transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                               German MS, Lin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-MAR-2001; 2001US-0817360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-SEP-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; transcription factor; neuroendocrine basic helix-loop-helix; type 2 diabetes mellitus; autoimmune destruction; type 1 diabetes; islet cell; cell therapy; neurogenin 1; Ngn1; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human neurogenin 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD46889 standard; DNA; 714 BP
                                                                                                          Sequence 714 BP; 118 A; 287 C; 207 G; 102 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-759853/82.
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                                                                   Similarity
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 GCGGCGCCGCGGACGCGGTCCGCTCCGAGGCGCTGCTGCACTCGCTGCGCAGGAG
                                                       Conservative
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/product= "Human Ngn1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Ngn1) gene #2.
                                                                 10.1%;
71.2%;
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                                                     Score 147.6; DB 24
Pred. No. 4.7e-30;
0; Mismatches 79;
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                                                              GACGCTGCGCCTACAACTACATCTGGGCTCTGGCCGAGACACTGCGCCTGGCGGA
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TCAAGGGCTGCCCGGAGGCGGTGCCCGGGAGCGC
                             CCACAGCTTCTACGGCCCCGAGCCCCCTGTGCCC
                                                                                            GACCCTGCGCTTCGCCCACAACTACATTTGGGCACTGACTCAGACGCTGCGCATAGCGGA
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455 886 395

Search completed: January 26, 2004, 19:39:01 Job time -: 430 secs

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Result
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/cgn2 6/ptcdata/2/ina/5B_COMB.seq:*
/cgn2 6/ptcdata/2/ina/6A COMB.seq:*
/cgn2 6/ptcdata/2/ina/6B COMB.seq:*
/cgn2 6/ptcdata/2/ina/BTUS COMB.seq:*
/cgn2 6/ptcdata/2/ina/backfiles1.seq:*
                             GenCore version 5.1.6 (c) 1993 - 2004 Compugen
                                                 US-08-932-411A-19
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US-08-932-411A-13
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05-07-753-520B-1	PCT-US94-12912-1	US-09-736-457-1798	US-09-702-705-1798	US-09-234-332-4	PCT-US95-05741-3	US-09-499-227-3	US-08-910-973-3	US-08-552-142A-3	PCT-US95-05741-10	PCT-US95-05741-8	US-09-499-227-8	US-08-910-973-8	US-08-552-142A-8	US-09-234-332-2	US-09-234-332-1	US-09-499-227-14	US-08-910-973-14
sequence i, Appii	٠,	17	Sequence 1798, Ap	Sequence 4, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 10, Appl	Sequence 8, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 14, Appl	Sequence 14, Appl

ALIGNMENTS

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RESULT 1
US-08-932-411A-19
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                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/932,411A FILING DATE: 15-SEP-1997 CLASSIFICATION: 536 PRIOR APPLICATION UNMBER: US 08/772,009 FILING DATE: 19-DEC-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Anderson,
APPLICANT: Ma, Qiufu
TITLE OF INVENTION: 1
                                                                                                                                                           TELEFAX: (415) 398-32-
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
                                             TOPOLOGY: un MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                        NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/722,570 FILING DATE: 19-DEC-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 804 base pairs
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            NAME/KEY:
LOCATION:
                                                                            COUNTRY:
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                                                                                                Sequence 12, Application US/08910973 Patent No. 5795723
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 731; Conservative
                                                                                     GENERAL INFORMATION:
                        APPLICANT: Tapscott, Stephen J.
APPLICANT: Olson, James M.
TITLE OF INVENTION: Expression
NUMBER OF SEQUENCES: 24
              CORRESPONDENCE ADDRESS
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; LOCATION:
US-08-910-973-12
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MOLECULE TYPE:
ORIGINAL SOURCE:
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Query Match
Best Local Similarity
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IMMEDIATE SOURCE:

TONE: 20A1 (neuroD3)
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US9
PILING DATE: 08-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/1
PILING DATE: 30-October-1996
ATTORNEY, AGENT INFORMATION:
NAME: Sheiness, Diana K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 206-225-0779 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1268 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 206-682-8100; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Sheiness, Diana K. REGISTRATION NUMBER: 35,356 REFERENCE/DOCKET NUMBER: FH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: dou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1420 Fifth Avenue, Suite 2800 CITY: Seattle
                                                                                                                                                                                                                                                                            CCGGCGCAAGAAGGCCAACGACCGGGGGGGGCGCAACCGCATGCACACACCTTAACTCCGCGCCT
                                                                                                                                                                                                                                                                                                                                                              GCGGCGCGGAGGGCGCAACAGGCCCAAGAGCGAGTTGGCACTGAGCAAGCCAGCGACGAAG
                                        CCACAGCTTCTACGGCCCCGAGCCCCCCTGTGCCC
                                                                                                         GACCCTGCGCTTCGCCCACAACTACATTTGGGCACTGACTCAGACGCTGCGCATAGCGGA
                                                                                                                                                                 GGACGCACTGCGCAGCGTGCCCTCGTTCCCCGACGACACCAAGCTCACCAAAATCGA
                                                                                                                                                                                                                                                                                                                                  GCGGCGCCGCGGACGCGGGTCCGCTCCGAGGCGCTGCTGCACTCGCTGCGCAGGAG
  TCAAGGGCTGCCCGGAGGCGCTGCCCGGGAGCGC
                                                                                                                                                                                                          GGATGCGCTGCGCGGCCCCCCCCTCCCGGATGACGCCAAACTTACAAAGATCGA
                                                                                                                                                                                                                                                     CCGGCGCGTCAAGGCCAACGATCGCGAGCGCAACCGCATGCACAACTTGAACGCGGCCCT
                                                                                 GACGCTGCGCTTCGCCTACAACTACATCTGGGCTCTGGCCGAGACACTGCGCCTGGCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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55..768
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 147.6; DB 1;
Pred. No. 1.1e-29;
D; Mismatches 79;
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543
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APPLICATION NUMBER: PCT/US96/17532

PILING DATE: 30-October-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/910,973

PILING DATE: 07-August-1997

ATTORNEY/AGENT INFORMATION:
NAME: Sheiness, Diana K.
REGISTRATION NUMBER: 35,356

REFERENCE/DOCKET NUMBER: 35,356

REFERENCE/DOCKET NUMBER: PHCR-1-12742

TELECOMMUNICATION INFORMATION:
TELEPAN: 206-225-0779
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                US-09-499-227-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/09499227
                                                                                                                                                                                                Matches 195;
                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Tapscott, Steph
APPLICANT: Olson, James M.
TITLE OF INVENTION: Expres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 05-August
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/239,238
FILING DATE: 06-May-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                  CLONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: WO PCT/US95/05741 FILING DATE: 08-May-1995
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                                                                                               CCGGCGCAAGAAGGCCAACGACCGGGAGCGCAACCGCATGCACAACCTTAACTCCGCGCT 766
                             GGATGCGCTGCGCGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAGATCGA 826
                                                                                                                                GCGGCGCCGCCGGACGCGGGTCCGCTCCGAGGCGCTGCTGCACTCGCTGCGCAGGAG
 GGACGCACTGCGCAGCGTGCTGCCCTCGTTCCCCGACGACACCAAGCTCACCAAAATCGA
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                                                                                                                                                                                            Score 147.6; DB of Pred. No. 1.1e-29 O; Mismatches 7
                                                                                                                                                                                                                             DB 4;
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Patent No. 6555337
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                                                                                                                                                                                                                                                                                                                                                               Matches
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-63
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 27-SEP-1996
CLASSIFICATION: 5365
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MEDIUM TYPE: Floppy
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TITLE OF INVENTION: 1
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STREET: Fo
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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875 GCGCATAGCGGACCACAGCTTCTACGGCCCCGGAGCCCCCCTGTGCCC 920
                                                                                                                                                                                                           516 GCTGCGGAGGAGCCGTCGCGTCAAGGCCAACGATCGCGAGCGCAACCGTATGCATAACCT
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                                                       636 CACCAAGATTGAGACGCTGCGCTTCGCCTACAACTACATCTGGGCCCTGGCTGAGACACT
                                                                                            815 TACAAAGATCGAGACCCTGCGCTTCGCCCACAACTACATTTGGGCACTGACTCAGACGCT 874
                                                                                                                                  576 CAACGCTGCGCTGGACGCTCTGCGCAGCGTGCTGCCCTCGTTCCCCGACGACACCAAGCT
                                                                                                                                                                                                                                               695 GCAGCGACGAAGCCGGCGCAAGAAGGCCAACGACCGGGAGCGCAACCGCATGCACAACCT
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                                                                                                                                                                                                                                                                                      TCAAGGGCTGCCCGGAGGCGCTGCCCGGGAGCGC 543
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                                                                                                                                                              TAACTCCGCGCTGGATGCGCGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACT 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1527 base pairs
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                                                                                                                                                                                                                                                                                                                                                             Score 145.2;
Pred. No. 4.8e
0; Mismatches
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Suite 3400
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696 GCGCCTGGCAGATCAAGGGCTCCCGGGGGGGCGCGGTGCCCCGGGAGCGC 741

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US-08-932-411A-12
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/772,009
FILING DATE: 19-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/722,570
FILING DATE: 19-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-63902-3/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEPHONE: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 398-324
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Anderson, APPLICANT: Ma, Qiufu TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1527 base pairs TYPE: nucleic acid STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 15 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
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                       875
                                                       636
                                                                                       815
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                                                                                                                                                                                                                                                   456 GCAGGAGCGGCGACGGCGAGGTCGCGCGCGGGTGCGGTCCGAGGCGCTGCTGCACTC
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198; Conserv
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5. 6566496
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     GCGCATAGCCGACCACAGCTTCTACCGCCCCCGAGCCCCCCTGTGCCC 920
                                                                              TACAAAGATCGAGACCCTGCGCGTTCGCCCACAACTACATTTGGGCACTGACTCAGACGCT 874
                                                                                                                                            TAACTCCGCGCTGGATGCGCTGCGCGGGTGTCCTGCCCACCTTCCCCGGATGACGCCAAACT
                                                         CACCAAGATTGAGACGCTGCGCTTCGCCTACAACTACATCTGGGCCCTGGCTGAGACACT
                                                                                                                       CAACGCTGCGCTGGACGCTCTGCGCAGCGTGCTGCCTCGTTCCCCCGACGACACCAAGCT
                                                                                                                                                                                     GCTGCGGAGGAGCCGTCGCGTCAAGGCCAACGATCGCGAGCGCAACCGTATGCATAACCT
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Pred. No. 4.8
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RESULT 7
US-08-932-411A-13
; Sequence 13, Application US/08932411A
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NESULT 6
US-08-722-570-13
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Best Local Similarity 68.2%;
Matches 195; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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LENGTH: 738 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
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NAME: Silva, Robin M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 38 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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STATE: California
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                                    GCGCATAGCGGACCACAGCTTCTACGGCCCCGAGCCCCCTGTGCCC
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GCGCCTGGCAGATCAAGGGCTCCCCGGGGGGCAGTGCCCGGGAGCGC
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N: 5365
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Pred. No. 7.2e-28;
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Suite 3400
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Best Local Similarity 68.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/
FILING DATE: 19-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,30
REFERENCE/DOCKET NUMBER: !
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INFORMATION FOR SEQ ID NO:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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LENGTH: 738 base pairs
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APPLICATION NUMBER: US 08/772,009
FILING DATE: 19-DEC-1996
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GCGCCTGGCAGATCAAGGGCTCCCCGGGGGGCAGTGCCCCGGGAGCGC 492
                                 GCGCATAGCGGACCACAGCTTCTACGGCCCCGAGCCCCCTGTGCCC 920
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Pred. No. 7.2e-28;
0; Mismatches 91; Indels 0
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US-08-910-973-21
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Patent No. 5795723
GENERAL INFORMATION:
                                                                                                                                                                                                                                      Best Local Similarity Matches 195; Conserv
                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/239,238
APPLICATION DATE: 06-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US95/057-
FILLING DATE: 08-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/17532
APPLICATION NUMBER: DCT/US96/17532
APPLICATION NUMBER: 30-OCCODER-1996
ATTORNEY/AGENT INFORMATION:
NAME: Shelness, Diana K.
REGISTRATION NUMBER: 35,356
REGISTRATION NUMBER: 35,356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 206-225-0779 INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER: PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mus musculus IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: FHCR-1-10958
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-682-8100; 206-224-0735 (direct)
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                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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CLASSIFICATION:
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                                     755 TAACTCCGCGCTGGATGCGCTGCGCGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACT 814
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  CAACGCTGCGCTGGACGCCTTGCGCAGCGTGCCTCGTTCCCCGACGACACCAAGCT
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1420 Fifth Avenue, Suite 2800
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                                                                                                                                                                                                                                                         9.6%;
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                                                                                                                                                                                                                                    Score 140.4; DB 1;
Pred. No. 8.6e-28;
0; Mismatches 91;
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US-09-499-227-21
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US-09-499-227-21
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Patent No. 6444463
GENERAL INFORMATION:
APPLICANT: Tapscott, Stephen J.
APPLICANT: Olson, James M.
                              Query Match
Best Local Similarity
Matches 195; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/
FILING DATE: 06-May-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT
FILING DATE: 08-May-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                              NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                     FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 1
FILING DATE: 05-Augus
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE POPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Expression of Neurogenic bHLH Genes in Primitive Neuroectoder NUMBER OF SEQUENCES: 24
                                                                                                                                                                                  ORGANISM: Mus musculus IMMEDIATE SOURCE:
                                                                                                                                                                                                                       MOLECULE TYPE: |
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: FHOME
                                                                                                                                                                                                                                                                        LENGTH: 1333 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                           COPOLOGY:
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635 GAAGCTCCGTGCGCGCGCGCGAGGGCCCAACAGGCCCAAGAGCGAGTTGGCACTGAGCAA 694
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                                Conservative
                                                                                                                                                                                                                                                           linear
                                                                                                                    101..835
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                                                                                                                                                                                                                                        DNA (genomic)
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07-August-1997
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                                              9.6%;
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                              0;
                                              Score 140.4; DB 4
Pred. No. 8.6e-28;
                                Mismatches
                                                                DB 4;
                                91;
                                                                Length 1333;
                                Indels
                              <u>,</u>
                            Gaps
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RESULT 10
US-08-932-411A-17
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                                                           US-08-932-411A-17
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Anderson, I APPLICANT: Ma, Qiufu TITLE OF INVENTION: NI NUMBER OF SEQUENCES:
                                                                                                                                                                                                                       TELEX: 910 277299
[NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/932,411A
                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 19-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 19-DEC-1996
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MEDIUM TYPE: Floppy disk
                                                                                                                                    MOLECULE TYPE:
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APPLICATION NUMBER: US 08/722,570
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                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
                                                                              NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                         NAME: Silva, Robin M. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                          TYPE:
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                                                                                                                                                                                  1: 1385 base pairs nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                  (415) 398-3249
                                                                            CDS
382..1170
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     9.6%;
78.1%;
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                                                                                                                                                                                                                                                                                                                                                           38,304
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     Score 139.8; DB 4; Pred. No. 1.3e-27;
                       Length 1385;
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RESULT 11
US-08-552-142A-12
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                                                                                                                                                                                                                                    TELEFAX: 206-225-0709 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: FHCR-1-8933
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-682-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: UFILING DATE: 02-NOV-1CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tapscott, Stranley M.
APPLICANT: Hollenberg, Stanley M.
                                                                                            MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 08-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/239,238
FILING DATE: 06-MAX-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US95/0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                       IMMEDIATE SOURCE:
NAME/KEY:
                                  CLONE:
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                                                                                                                                                        STRANDEDNESS:
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                                                                              ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                     Broderick, Thomas F.
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Tapscott, Stephen J.
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                                                                          Homo sapiens
                                                                                                                                 linear
                                                                                                                 DNA (genomic)
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RESULT 12
US-08-722-570-14
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                                                                    ; TOPOLOGY: ur
; MOLECULE TYPE:
US-08-722-570-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-552-142A-12
Query Match
Best Local Similarity
Matches 163; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/08722570 Patent No. 6555337
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                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1312 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,570
FILING DATE: 27-SEP-1996
CLASSIFICATION: 5365
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                         TELEFAX: (415) 398-3249
TELEX: 910 277299
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Four Embarcadero Center,
7.9%; ilarity 67.4%; Conservative
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65.2%;
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                                                                                                                                                                                         14:
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 Score 115.6; DB Pred. No. 3.1e-210; Mismatches 7
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Pred. No. 4.6e-23;
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                                 DB 4;
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   Indels
                                 Length
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STRANDEDNESS:
TOPOLOGY: unkr
MOLECULE TYPE: I
US-08-932-411A-15
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US-08-932-411A-15
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                                                                                                                                    TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS:
LENGTH: 1312 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6566496
GENERAL INFORMATION:
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Query Match 7.9%;
Best Local Similarity 67.4%;
Matches 163; Conservative
                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/772,009
FILING DATE: 19-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/722,570
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                                                                                                                                                                                                                                            NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-63902-3/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                FILING DATE: 19-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/932,411A
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                                                                                                                                                                                                               TELEPHONE: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 15
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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94111-4187
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                                                                                                         unknown
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                                                                                                                                                                                             15:
 Score 115.6; DB 4;
Pred. No. 3.1e-21;
0; Mismatches 79;
                                  DB 4;
                                   Length
     Indels
                                   1312;
   <u>.</u>
   Gaps
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RESULT 14
US-08-722-570-15
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15, Application US/08722570 Patent No. 6555337
                                                                                                                                 Query Match
Best Local Similarity
                                                                                                              Matches 138;
                                                                                                                                                                                                                                                                                 TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1277 base pairs
                                                                                                                                                                                                                                                                                                                                                       NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-63
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Anderson, APPLICANT: Ma, Qiufu TITLE OF INVENTION: 1
                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test,
STREET: Four Embarcadero Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 27-SEP-1996 CLASSIFICATION: 5365
                                                                                                                                                                                                                             STRANDEDNESS:
TOPOLOGY: un
                                                                                                                                                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94111-4187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             719 GACCTTGCGCTTTGCCTACAACTACATCTGGGCTCTTAGCGAAACTTTGCGCCTTGGCGA
765 CTGGATGCGCTGCGCGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAGATC 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACCCTGCGCTTCGCCCACAACTACATTTGGGCACTGACTCAGACGCTGCGCATAGCGGA 886
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                                                                         AGCCGGCGCAAGAAGGCCAACGACCGGGAGCGCAACCGCATGCACAACCTTAACTCCGCG
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                                                                                                                Conservative
                                                                                                                                                                                                                                unknown
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ur Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                unknown
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                                                                                                                                 74.68;
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                                                                                                                                                                                                                                                                                                                          15:
                                                                                                            Score 109.8; DB 4;
Pred. No. 1e-19;
0; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                     A-63902/RFT/RMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Version #1.30
                                                                                                              47;
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                                                                                                                Gaps
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ACTTA	765 CTGGATGCGCTGCGCGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAGATC
CCTTA	705 AGCCGGCGCAAGAAGGCCAACGACCGGGAGCGCAACCGCATGCACAACCTTAACTCCGCG
1 1277;	Query Match 7.5%; Score 109.8; DB 4; Length Best Local Similarity 74.6%; Pred. No. 1e-19; Matches 138; Conservative 0; Mismatches 47; Indels
	910 277299 FOR SEQ ID N HARACTERISTI 1277 base p ucleic acid NESS: unknown TYPE: DNA
	TRATION N ENCE/DOCK MUNICATIO HONE: (4
	APPLICATION UNMER: US 08/722,570 FILING DATE: 19-DEC-1996 ATTORNEY/AGENT INFORMATION: NAME: Silva Robin M.
	SSIFICATI APPLICAT LICATION LI
	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/932,411A FILING DATE: 15-SEP-1997
	R READA
	CII: Sdiffernia STATE: California COUNTRY: United States ZIP: 94111-4187
LLP	31 : hbach Test Albritton & Herbert adero Center, Suite 3400
	619 GACCA 623
	885 GACCA 889
CTTTGC	825 GAGACCCTGCGCTTCGCCCACAACTACATTTGGGCACTGAGACGCTGCGCATAGCG
AAACTCAC	

Search completed: January 26, 2004, 22:06:42 Job time : 100 secs

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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         900.6
682.4
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seq length: 2000000000
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1: /cgn2 6/ptodata/1/pubpna/US07 PUBCOMB.seq:*

2: /cgn2 6/ptodata/1/pubpna/PCT_NEW PUB.seq:*

3: /cgn2 6/ptodata/1/pubpna/US06_NEW PUB.seq:*

4: /cgn2 6/ptodata/1/pubpna/US07_NEW PUB.seq:*

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6: /cgn2 6/ptodata/1/pubpna/US08_NEW PUB.seq:*

6: /cgn2 6/ptodata/1/pubpna/US08_NEW PUB.seq:*

8: /cgn2 6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2 6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2 6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

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18: /cgn2 6/ptodata/1/pubpna/US10B_UBCOMB.seq:*

18: /cgn2 6/ptodata/1/pubpna/US00_NEW_PUB.seq:*
                                                                                                                                                                                                                                                                                                  Match
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       gcaggtagcgagagcag.....agagtgacctaatccagtgt 1460
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       1861
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1790
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1277
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         114
144
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   4 US-10-004-717-30

4 US-10-004-717-6

4 US-10-004-717-37

4 US-10-004-717-20

4 US-10-004-717-18

US-008-722-570-14

US-08-722-570-14

US-08-722-570-13

US-10-413-358-26
                                                                                                                                                                  4 US-10-004-717-24

4 US-10-004-717-4

US-09-817-360-1

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US-08-722-570-13
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Sequence 3, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 13, Appl
Sequence 30, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 20, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 27, Appl
Sequence 27, Appl
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	-10-02/-032-10123 -10-135-337-56	-10-027-633	-10-027-632-10123	-10-029-386-	-10-004-717-	0-004-717-	-10-004-717	7	0-004-717-	-10-004-717-	US-09-908-975-30269	0-004-717-	4-717-	US-10-157-031-238	-09-	9-749-728B-2	27-632-	0-027-632-9728	-10-027-632-9728	-10-027-63	0-027-632-9728	-10-027-632-9728	9-908-975-	4-090-2	9-749-728B-2	0-004-717	US-10-004-717-39	9-833-381-	7-	17-1
	א ני	_	e 101	e 227	e 45,	e 10,	e 57,	e 1,	e 65,	e 15, App	e 30	е 8	e 43	e 23	e 35	e 24,	e 97	e 972	e 972	e 972	e 972	e 972	e 414	e 251	e 22,	e 22,	е 39,	e 508	e 59,	ω

ALIGNMENTS

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                                                                                                                                                                                                                            Matches 1094;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/817,360
CURRENT FILLING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/535,145
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 60/128,180
PRIOR FILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: German, Michael S.
APPLICANT: Lin, Joseph
TITLE OF INVENTION: PRODUCTION OF PANCREATIC ISLET CELLS
TITLE OF INVENTION: AND DELIVERY OF INSULIN
FILE REFERENCE: UCSF-129CIP
                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0
123 ATT----AGCAGCTCAGAAGTCCCTCTGGGTCTCACCACTGCA-CAGAGGCCGAGGACCC 177
                                                                 654 GCCCGGCAGGCACGCTCCTGGCCGGGGGCAGAGCAGATAAAGCGTGCCAGGGGGACACACG
                                                                                                                                              64 GCCCGGCAGGCACGCTCCTGGTC-CGGGCAGAGAGAGATAAAGCGTGCCAGGGGACACACG 122
                                                                                                                                                                      GGTAGCGAGAGGAGCAGTCCCTGGGCCCCCGTTGCTGATTGGCCCCGTGGCACAGGCAGCA 63
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                                                                                                                                                                                                                                             61.7%;
86.2%;
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                                                                                                                                                                                                                          Score 900.6; DB 9;
Pred. No. 4.5e-248;
0; Mismatches 129;
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CCCCAGTTTCCCAAGCTGGTAGCCTGAGCCCCACAGCCTCATTGGAGGAGTTCCCTGGCC
                                                                                                                                                                                                                                                  CACTGACTCAGACGCTGCGCATAGCGGACCACAGCTTCTATGGCCCCGGAGCCCCCTGTGC
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PRIOR APPLICATION NUMBER: 60/176,993
PRIOR APPLICATION NUMBER: 60/176,993
PRIOR APPLICATION NUMBER: 60/137,060
PRIOR APPLICATION NUMBER: 60/137,060
PRIOR APPLICATION NUMBER: 60/137,060
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 69
SOPTWARE: PRIENTIN Ver. 2.1
SEQ ID NO 24
LENGTH: 861
TYPE: DNA
ORGANISM: Mus musculus
US-10-004-717-24
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Publication No. US20020192665A1

GENERAL INFORMATION:
APPLICANT: ZOGHBI, HUDA Y.
APPLICANT: YANG, QI
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE TITLE OF INVENTION: ATONAL ASSOCIATED SEQUENCE FOR DEARNESS, TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION FILE REFERENCE: PO1899US4
CUURRENT APPLICATION UNMER: US/10/004,717
CUURRENT FILING DATE: 2002-08-16
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Best Local
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Local Similarity 89.7%;
les 771; Conservative
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US-10-004-717-4
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                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/176,993
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: 60/137,060
PRIOR FILING DATE: 1999-06-01
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CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/585,645
PRIOR FILING DATE: 2000-06-01
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APPLICANT: YANG, QI
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE
TITLE OF INVENTION: ATONAL ASSOCIATED SEQUENCE FOR DEAFNESS,
TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn Ver. 2.1
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 CGACGAAGCCGGCGCAAGAAGGCCCAACGACCGGGAGCGCAACCGCATGCACAACCTTAAC
                                   CTCCGCGCCCGACGCGGAGGGCGCAACAGGCCCAAGAGCGAGTTGGCACTCAGCAAACAG
                                                     CTCATACCTAGGGACTGCTCCGAAGCAGAAGTGGGTGACTGCCGAGGGACCTCGAGGAAG
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US-09-817-360-1
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APPLICANT: German, Michael S.
APPLICANT: Lin, Joseph
TITLE OF INVENTION: PRODUCTION OF PANCREATIC
TITLE OF INVENTION: AND DELIVERY OF INSULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version SEQ ID NO 1
LENGTH: 5340
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                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 826; Conserv
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CURRENT FILLING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/535,145
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 60/128,180
PRIOR FILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 19
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 241 CAAAACTTCGAAGCGAGCAG-----
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                                                           CGAGCTTCTTTGCTGCCTCCAGACGCAATTTACT-CCAGGCGAGGGCGCCTGCAGCTCAG
                                                                                                         TCCCTGCGGTCTCACCGCCGCGCCCTCGAGAGAGAGGCGTGACAGAGGCCTCGGACCCCATT
                                                                                                                               CCCTCTGGGTCTCACCACTGC-----
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                                   CTCTCTTCTTTTCTCCTTTGGGGCTGGGGCAACTCCCAGGCGGGGGGGCCCTGCAGCTCAG
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                                                                                                                                                                                                                                                                                                                       Score 517.4; DB 9;
Pred. No. 4.5e-138;
0; Mismatches 351;
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 -- AGGGGTTCAGCTATCCACCGCTGCT 285
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5340 48;

Gaps

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240

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645

540

600

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420

480

360

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RESULT 5
US-08-722-570-12
; Sequence 12, Application US/08722570
; Publication No. US20030044887A1
; GENERAL INFORMATION:
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                                                                                                                                           AAGGTAGTGGAGGCACTCGAGCATC 1196
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                                                                                                                                                                                                                                                                                                 GGCTGGCAGCCTGAGTCCCGCCGCGTCGCTGGAGGAGCGACCCGGGCTGCTGGGGGGCCAC
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                                                                                                                                                                                                                                                                                                                                                           GCTGGGCAGCCCAGGCGGTTCCCCCGGGGACTGGGGGTCCCTCTACTCCCCAGTCTCCCA
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                                                                                                             AGGGTGGCCGACGGCGGCGGCCCTC
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TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 1527 base pairs
TYPE: nucleic acid
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Best Local 9
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CLASSIFICATION: 5365
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-63
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ma, Qiufu
TITLE OF INVENTION: NEUROGENIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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hes 198; Conserv
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                                        GCGCATAGCGGACCACAGCTTCTACGGCCCCGAGCCCCCTGTGCCC
                                                                                  CACCAAGATTGAGACGCTGCGCTTCGCCTACAACTACATCTGGGCCCCTGGCTGAGACACT
                                                                                                                                                                 CAACGCTGCGCTGGACGCTCTGCGCAGCGTGCTGCCCTCGTTCCCCGACGACACCAAGCT
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GCGCCTGGCAGATCAAGGGCTCCCGGGGGGGGGGCGTGCCCGGGAGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                             Score 145.2; DB 8;
Pred. No. 2e-31;
0; Mismatches 88;
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RESULT 6
US-08-722-570-13
                                                                                                          Sequence 13, Application US/08722570 Publication No. US20030044887A1 GENERAL INFORMATION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
ADDRESSEE: Flehr, H
                                                     APPLICANT: Anderson,
APPLICANT: Ma, Qiufu
TITLE OF INVENTION: 1
                                                         NEUROGENIN
 Hohbach, Test, Albritton & Herbert
                                                                                            David
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635

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RESULT 7
US-10-004-717-30
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TELEFAX: 910 277299
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
LENGTH: 738 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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                                                                                                                                                                                                                                         Sequence 30, Application US/10004717 Publication No. US20020192665A1 GENERAL INFORMATION:
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Best Local Similarity 68.2%;
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF TITLE OF INVENTION: ATOMAL ASSOCIATED SEQUENCE FOR DEAFNESS,
TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION FILE REFERENCE: P01899US4
CURRENT APPLICATION NUMBER: US/10/004,717
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/585,645
PRIOR PILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: 60/176,993
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FILING DATE: 27-SEP-1996
CLASSIFICATION: 5365
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-63902/RFT
                                                                                                                                                                                                 APPLICANT: ZOGHBI, HI APPLICANT: YANG, QI
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEPAX: (415) 398-3249
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TOPOLOGY: unknown
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Pred. No. 4.1e-30;
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; LENGTH: 1385
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; ORGANISM: Mus musculus
US-10-004-717-30
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                                                                                                                                                                                                                                                Query Match
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CURRENT APPLICATION NUMBER: US/10/004,717
CURRENT FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
PRIOR PRIOR PRIOR DESCRIPTION NUMBER: 60/176,993
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 2000-01-19
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PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                       LENGTH: 1412
TYPE: DNA
ORGANISM: Mus musculus
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GAGACGCTGCGCTTCGCCCACAATTACATCTGGGCGCTCACCGAGACTCTGCGCCTGGCG
                    GAGACCCTGCGCTTCGCCCACAACTACATTTGGGCACTGACTCAGACGCTGCGCATAGCG
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Pred. No. 7e-30;
0; Mismatches
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RESULT 10
US-10-004-717-20
Sequence 20, Application US/10004717
Publication No. US20020192665A1
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US-10-004-717-37
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US-10-004-717-37
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Best Local Similarity
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APPLICANT: YANG, QI

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF
TITLE OF INVENTION: ATONAL ASSOCIATED SEQUENCE FOR DEAFNESS,
TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION
                                                           FILE REFERENCE: P01899US4
CURRENT APPLICATION NUMBER: US/10/004,717
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/585,645
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: 60/176,993
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CURRENT APPLICATION NUMBER: US/10/004,717
CURRENT FILING DATE: 2002-08-16
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TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION
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PRIOR TILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: 60/176,993
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: 60/137,060
PRIOR FILING DATE: 1999-06-01
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78.1%;
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; TYPE: DNA
; ORGANISM: chicken
US-10-004-717-20
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US-10-004-717-18
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SEQ ID NO 18
LENGTH: 1074
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18, Application US/10004717
Publication No. US20020192665A1
GENERAL INFORMATION:
APPLICANT: ZOGHBI, HUDA Y.
APPLICANT: YANG, QI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn Ver. 3
SEQ ID NO 20
LENGTH: 790
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Best Local Similarity
Matches 156; Conserv
                                                                                                                                                                                                                                                  Matches 182;
                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/137,060 PRIOR FILING DATE: 1999-06-01 NUMBER OF SEQ ID NOS: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/004,717
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/585,645
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: 60/176,993
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 2000-01-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE TITLE OF INVENTION: ATONAL ASSOCIATED SEQUENCE FOR DEAFNESS, TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: P01899US4
                                                                                                                                                                                                                                                                                                                                           ORGANISM: chicken
                                                                                                                                                                                                                                                                      Local Similarity
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822
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ATCGAGACCCTGCGCTTCGCCCACAACTACATTTGGGCACTGACTCAGACGCTGCGCATA 881
                                                                  GCGCTGGATGCGCTGCGCGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAG
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                                                                                                         CGGAGCCGCCGGGTGAAAGCCAACGACCGGGAGCGGAACCGCATGCACCACCTCAACGCC
                                                                                                                                                                              CGGCGGAGGAGACGCGGCGGGCGGGGCGCGGACCGAGGCTTTGCTGCACACCCCTCAAA
                                     GCGCTGGATGAGCTCCGCAGCGTCCTGCCGACCTTCCCCGACGACACCAAACTCACCAAA
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Pred. No. 1.9e
0; Mismatches
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Pred. No. 9.3e-30;
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US-08-722-570-14
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Publication No.
                                                                                                                                                                                                                                                                                                                   Matches 163;
                                                                                                                                                                                                                                                                                                                                 Query Match 7.9%;
Best Local Similarity 67.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGINT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-63902/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEPAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NEUROGENIN NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Anderson, APPLICANT: Ma, Qiufu
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CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/722,570 FILING DATE: 27-SEP-1996 CLASSIFICATION: 5365
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States ZIP: 94111-4187
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TOPOLOGY: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
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779
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                                                                                                                                                                                                                                                    GAGGAGCCGAGGCCGCGCTCAGGGCAAGAGCGGAGAAACTGTGTTAAAGATCAAGAAGAC
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                            CC 888
                                                              GACCTTGCGCTTTGCCTACAACTACATCTGGGCTCTTAGCGAAACTTTGCGCCTTGGCGA 778
                                                                                         GACCCTGCGCTTCGCCCACAACTACATTTGGGCACTGACTCAGACGCTGCGCATAGCGGA 886
                                                                                                                          TGATTCCCTCAGGGAAGTGTTGCCCCTCTTTACCTGAAGATGCCCAAACTCACCAAGATAGA
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                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                unknown
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                                                                                                                                                                                                                                                                                                                Score 115.6; DB Pred. No. 6e-23; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                               DB 8;
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; Sequence 15, Application US/08722570
Publication No. US20030044887A1
; GENERAL INFORMATION:
APPLICANT: Anderson, David J.
APPLICANT: Ma, Qiufu
TITLE OF INVENTION: NEUROGENIN
NUMBER OF SEQUENCES: 20
                                US-10-413-358-27
; Sequence 27, Application US/10413358
; Publication No. US20030219894A1
; GENERAL INFORMATION:
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US-08-722-570-15
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                                                                                                                RESULT 14
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US-08-722-570-15
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
APPLICANT: Susumu Seino, JCR Pharmaceuticals Co., I TITLE OF INVENTION: Induction of insulin-producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-63
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE: 27-SEP-1996
CLASSIFICATION: 5365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                          619
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                                                                                                                                                                                                                885 GACCA 889
                                                                                                                                                                                                                                                                                                                                                                                                                                              705 AGCCGGCGCAAGAAGGCCAACGACCGGGAGCGCAACCGCATGCACAACCTTAACTCCGCG
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                                                                                                                                                                                                                                                      GAGACCTTGCGCTTTGCCCCACAACTACATCTGGGCTCTTAGCGAAACTTTGCGCCTGGCC
                                                                                                                                                                                                                                                                                                                              CTCGATTCTCTGAGGGAGGTTCTACCGTCATTACCCGAAGACGCCAAACTCACCAAGATA 558
                                                                                                                                                                                                                                                                              GAGACCCTGCGCTTCGCCCACAACTACATTTGGGCACTGACTCAGACGCTGCGCATAGCG 884
                                                                                                                                                                                                                                                                                                                                                        CTGGATGCGCTGCCGGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAGATC 824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 109.8; DB 8 Pred. No. 2.8e-21; 0; Mismatches 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Albritton & Herbert
Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 8;
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FILE REFERENCE: GP55

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CURRENT APPLICATION NUMBER: US/10/413,358;
CURRENT FILING DATE: 2003-04-15;
PRIOR APPLICATION NUMBER: JP2002-115064;
PRIOR FILING DATE: 2002-04-17;
NUMBER OF SEQ ID NOS: 27;
SEQ ID NO 27;
LENGTH: 1099;
TYPE: DNA;
ORGANISM: Homo Sapiens
US-10-413-358-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
US-10-413-358-26
; Sequence 26, Application US/10413358
; Publication No. US20030219894A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 26
LENGTH: 1211
TYPE: DNA
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Best Local Similarity
Matches 143; Conserv
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TITLE OF INVENTION: Induction of insulin-producing cells
FILE REFERENCE: GP55
CURRENT APPLICATION NUMBER: US/10/413,358
CURRENT FILING DATE: 2003-04-15
PRIOR APPLICATION NUMBER: JP2002-115064
PRIOR PILLING DATE: 2002-04-17
NUMBER: OF SEQ ID NOS: 27
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                             Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                         Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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1540 bp mRNA linear HTC 05-DEC-2002 Mus musculus adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010001M19 product:atonal homolog 5 (Drosophila), full insert sequence.
                                                                                                                                                       Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 99279253
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                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Group Phase I & II Team.
Analysis of the mouse transcriptome based on of 60,770 full-length cDNAs
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                       Encyclopedia Project of Genome Exploration Research Group in Riker Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAGGATCCAAGAGCTCTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 420, 563-573 (
6 (bases 1 to 1540)
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                                                                                                                                                                                                                      cDNA library was prepared and sequenced in Mouse Genome
                                                                                                                                                                                                                                                                 Please visit our web site (http://genome.gsc.riken.go.jp/) further details.
                                                                                                                                                                                                                                                                                                                                           Fax:81-45-503-9216)
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                      CTCAGTTCCAATTCCACCCCACCCTAGCCCCACTCTCGTACCGAGGGACTGCTCCGAAGCA 605
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/clone_Tib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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77.7%;
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                                                                                                                                            BY708009 1025 bp mRNA linear EST 16-DEC-2
BY708009 RIKEN full-length enriched, adult male small intestine
musculus cDNA clone 2010001M19 5', mRNA sequence.
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                Mus musculus
                                                                      Mus musculus (house mouse)
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RES Okazaki, Y., Furumo, M., Kasukawa, T., Machi, J., Bono, H., Kyondo, S., Nikidio, I., Osato, N., Salto, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hanegawa, Y., Nogami, A., Schonbach, C., Sogobori, T., Baldarell, R., Hill, D.P., Blit, C., Hume, D.A., Ogobori, T., Baldarell, R., Hill, D.P., Blit, C., Hume, D.A., Schonbach, Y., Balkay, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batadow, S., Galeiel, R. W., Blake, J.A., Bradh, D., Branis, C., Chothia, C., Cootret, J. B., Cousin, R., W., Blake, J.A., Bradh, D., Branis, C., Chothia, C., Cootret, J. B., Cousin, R., Schonbach, C., Chothia, C., Cootret, J. B., Charley, R. J., Scholl, R. J., Kanapin, A., Matsuda, H., Batadow, S., Salto, K., Wall, R. J., W
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/clone="2010001M19"

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="small intestine"
/dev_stage="adult"
/lab_host="SOLR"
/clone_lib="RIKEN full-length enriched,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . cDNA was cleaved with XhoI and SstI." 316 \text{ c} 286 \text{ g} 207 \text{ t} 1 \text{ others}
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                                                                                                                                                                                                                                                                              Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 160 row: G column: 18
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Contact: Shaying Zhao
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and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-23
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Mammalia; Eutheria;
                                                                                                                                                                                                                                           Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 593)
                                                                                                                                                                                                                                                               primer: T7
/clone_lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector:
                                                                                                                               /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                 ocation/Qualifiers
                          /lab_host="DH10B"
/clone_lib="RPCI-23"
                                                                    'sex="Female"
                                                                                          clone="RPCI-23-160G18"
                                                                                                              db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tsegaye, G., Geer, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               å
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             musculus
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      pBACe3.6; Site_1:
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e RPCI-23-160G18
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RESULT 4
CA945402
LOCUS
DEFINITION
                                  REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                   48
                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 687)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                       087 bp
UI-M-FDO-cdh-1-12-0-UI.r1 NIH BMAP
IMAGE: 6828925 5', mRNA sequence.
CA945402
                                  Unpublished
Contact: Robert Strausberg,
                                                                                                                                                                                                                  CA945402
CA945402.1 GI:27433882
                                                                                                                                                               Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                     GGCTC--ATCACTCCCCAGTCTCCCAAGCGGGAACCTAGCCCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                      GGCTCTATCTACTCCCCAGTTTCCCCAAGCTGGTAGCCTGAGCCCC 1010
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                                                                                                                                                                              musculus (house mouse)
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cgapbs-r@mail.nih.
Procurement: Dr. J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECORI; Site 2: ECORI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI methylase. Size selected DNA was cloned into the pBACe3.6 vector at the ECORI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
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91.5%;
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Pred. No. 1.8e-105;
O; Mismatches 46;
James Lin,
                    gov
                                    Ph.D
                                                                                                                                                                                                                                                                   P_FD0
Univeristy of Iowa
                                                                                                                                                                                                                                                                                          mRNA
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                                                                                                                                                                                                                                                                       linear
musculus
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VERSION
KEYWORDS
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AL540071
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ORIGIN
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                                                                                                                                                                                                                                                      rocus
                                                                                         ORGANISM
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Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 1001)
Li,W.B., Gruber,C., Jessee,J.
                                                                                                                                                                                  AL540071
AL540071 Homo sapiens FETAL BRAIN Homo sapiens CSODF035YD19 5-PRIME, mRNA sequence.
                                                                                                                                                          AL540071
AL540071.2 GI:31264632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                          EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: pYX-5
                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library preparation: Dr. M. Bento Soares, University of CDNA Library Arrayed by: Dr. M. Bento Soares, University of I DNA Sequencing by: Dr. M. Bento Soares, University of I Owa Clone Distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                            GAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                GAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGACGCTGCGCTTCGCCCACAATTACATCTGGGCGCTCACCGAGACTCTGCGCCTGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCCGCAGGCTCAAGGCCAACAACCGCGAGCGCAACCGCATGCACAACCTAAACGCCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNa was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TGAGAGAGCC. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Instututes of Mental Health
(NINMI), Hemin Chin, Ph.D., program coordinator."

17 a 228 c 250 g 91 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                            887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="whole brain"
/dev stage="embryo 12.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/lab_host="DH10B (T1 phage resistant)"
/clone lib="NIH BMAP FD0"
/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA
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83.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 133.4; DB 14; Pred. No. 5.1e-22; 0; Mismatches 31;
                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Best Local :
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BJ010277.1 GI:
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
On Feb 15, 2001 the
Contact: Genoscope
                                                                                                                                                                             Oryzias latipes (Japanese medaka)
Oryzias latipes
Cryzias latipes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
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BP 191 91006 EVRY cedex - France
Unpublished
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, u
Tel: 81-559-81-6856
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BJ010277 MF01SSA cDNA Oryzias
                                                                                                                       Kohara,Y., Shin-i,T., Kimura,T., N
Medaka EST Project in Takeda's lab
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/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo (dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and ECORV sites of the pCMVSPORT 6
vector. Library was not normalized."

322 c 342 g 121 t 26 others
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/tissue_type="FETAL BRAIN"
/dev_stage≑"fetal"
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/mol_type="mRNA"
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Pred. No. 7.5e-22;
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Best Local (
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                                                                                                                                                                                                                                                                                  1 (bases 1 to 600)

Mt,X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W. White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H. Gene expression in the developing mouse retina by EST sequence and microarray analysis

Nucleic Acids Res. 29 (24), 4983-4993 (2001)
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Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                   Department of Biochemistry and Molecular Biology University of Texas M.D. Anderson Cancer Center Box 117, 1515 Holcombe Blvd., Houston, TX 77030, Tel: 713 792 3646
Fax: 713 790 0329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BG808248 600 bp
2083-52 Mouse El4.5 retina lambda
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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/clone_lib="MF018SA cDNA"
231 c 190 g 90 t 1 c
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/sex="mixture of female and male"
/tissue_type="whole embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryzias latipes"
/mol_type="mRNA"
/strain="Hd-rR"
 /dev_stage="embryonic day 14.5
/clone_lib="Mouse_E14.5 retina
238 c 161 g 107 t
                                                                                                                 1. .600
                                                                  /mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                  Location/Qualifiers
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                                                                                                   organism="Mus musculus"
                                                    tissue_type="neural retina"
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Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UI-M-FR0-cbc-k-21-0-UI.rl NIH BMAP FR0 MUI-M-FR0-cbc-k-21-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BU612495.1 GI:23278710
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: pYX-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
1 (bases 1 to 730)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BU612495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGGAGCGCAACCGCATGCACAACCTTAACTCCGCGCTGGATGCGCTGCGCGGTGTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCCAGGGGGC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCCCTGTGCC 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACATCTGGGCGCTCACCGAGACTCTGCGCCTGGCGGACCACTGCGCCGGCGGCGGTGGC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   musculus (house mouse)
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/tissue type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH108 [71 phage resistant)"
/clone_lib="NIH_BMAP_FR0"
/clone_lib="NIH_BMAP_FR0"
/note="Organ: Brain; Vector: pyx- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel: First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pyx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
                                                                                                                                                                                                                                                                                                                                                                                                  clone="UI-M-FR0-cbc-k-21-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                mol_type="mRNA"
strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bento Soares, bento-soares@uiowa.edu was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                             xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.8%;
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Pred. No. 7.3e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissue Procurement: Dr. James Lin, Univeristy of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Rodentia; Sciurognatni; Muriuae; Muriuae, 1 (Dases 1 to 823)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
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UI-M-FD0-bzj-i-24-0-UI.rl NIH_B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BU054481.1 GI:22494558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMAGE: 6404447 5', mRNA sequence
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/db_xref="taxon:10090"
/cloine="IMAGE:6404447"
/tissue_type="whole brain"
/tissue_type="whole brain"
/dev_stage="embryo 12.5 dpc"
/lab_host="DH108 (TI phage resistant)"
/lab_host="DH108 (TI phage resistant)"
/cloine_lib="NH108 (TI phage resistant)"
/cloine_lib="NH108 (TI phage resistant)"
/cloine_lib="NH108 (TI phage resistant)"
/site_2: Not I; The library was constructed according to
Sonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNa was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   program coordinator.
a 244 c 264 g
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                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"

mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                        strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
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81.4%;
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BMAP_FD0 Mus musculus cDNA clone
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BX419330 Homo sapiens FETAL BRAIN Homo sapiens
CSODF015YD06 5-PRIME, mRNA sequence.
BX419330
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2626.r
Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitrogen.Corporation 1600
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1 (bases 1 to 947)
Li,W.B. Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens
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                                                                                                    /clone lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pcMVSPPGF 6; lst strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV stres of the pcMVSPORT 6
vector. Library was not normalized."
393 c 315 g 130 t 36 others
                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF015YD06"
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/dev_stage="fetal"
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BU924937
BU924937.1 GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Biochemistry and Molecular University of Texas M.D. Anderson Cancer Box 117, 1515 Holcombe Blvd., Houston, TX Tel: 713 792 3646
Fax: 713 790 0329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mu,X., Zhao,S., Pershad,R., Hsieh,T.-F., White,R.A., Beremand,P.D., Thomas,T.L., Gene expression in the developing mouse:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and microarray analysis
Nucleic Acids Res. 29 (
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Mammalia; Eutheria; Rodentia;
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                       CGGACCACAGCTTCTACGGCCCCGAGCCCCCTGTGCC
                                                           GAGACGCTTGCGCCTTTCGCCCCACAATTACATCTGGGCGCTCACCGAGACTCTGCGCCTGG
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                                                                                                                                                                                                                                                                                                                                  /tissue_type="neural retina"
/dev stage="embryonic day 14.5 post-fertilization"
/clone_lib="Mouse_E14.5 retina lambda_ZAP_II_Library"
/clone_lib="Mouse_E14.5 retina lambda_ZAP_II_Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe and Dr. Mina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CA979119 932 bp
AGENCOURT 11295215 NIH MGC 164 Mus
IMAGE: 30146192 5', mRNA sequence.
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National Institutes of Health, M
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Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                             CAACGCTGCGCTGGACGCCTTGCGCAGCGTGCTGCCCTCGTTCCCCGACGACACCAAGCT
                                                                                                                                                                                               TAACTCCGCGCTGGATGCGCTGCCGGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACT
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                                                                              CACCAAGATTGAGACGCTGCGCTTCGCCTACAAACTACATCTGGGGCCCTGGCTGAGACA 703
                                                                                                                                                                                                                                                                               GCAGCGACGAAGCCGGCGCAAGAAGGCCCAACGACCGGGAGCGCAACCGCATGCACAACCT 754
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CTGCGCCTGGCAGATCAAGGGCTCCCCGGGGGGCAGTGCCCCGG 746
                                    CTGCGCATAGCGGACCACAGCTTCTACGGCCCCGAGCCCCCTG
                                                                                                                  TACAAAGATCGAGACCCTGCGCTTCGCCCACAA--CTACATTTGGGCACTGACTCAGACG 872
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(bases 1 to 932)
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/db xref="vaxon:10090"

/clone="IMAGE:30146192"

/lab host="DH108 (phage-resistant)"

/lab host="DH108 (phage-resistant)"

/clone lib="NIH MGC 164"

/clone lib="NIH MGC 164"

/clone myector: pcMy-SpORT6.1.ccdb; Site_1: EcoRV; Site_2:

/note="wector: pcMy-SpORT6.1.cdb; Site_1: EcoRV; Site_2:

/note mouse embryonic limb, maxilla and mandible, day

pooled mouse embryonic limb, maxilla and mandible, day

10.5 and 11.5 (size selected for the 0.5-1 kb fragments)

Cloned directionally, priming method: Oligo-dT. cDNA

enrichment: >lk bp, Average insert size 1.8k bp. Priming

sequence: 5'GACTAGTTCTAGATCGCGACCGCCCC(T) 3'. Tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contributed by, David Rowe. Library constructed by ResGen.
Invitrogen Corp."
1 349 c 276 g 153 t 1 others
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20296633
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062M23 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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BP 191 91006 EVRY cedex - FRANCE
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  CGCATAGCGGACCA 889
                                                                            ACAAAGATCGAGACCCTGCGCTTCGCCCACAACTACATTTGGGCACTGACTCAGACGCTG 875
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/note="Genoscope sequence
/note="Genoscope sequence
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/mol_type="genomic DNA"
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(E-mail : seqref@genoscope.cns.
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Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing Center
Seq primer: -40RP from Gibco
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
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AW147434.1 GI:6195330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Sandy Clifton, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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                                      AAGCCGGCGCAAGAAGGCCAACGACCGGGAGCGCAACCGCATGCACAACCTTAACTCCGC 763
   AACCCGGCGCGTTAAAGCCAATAACCGCGAGAGGAATCGCATGCACCACCTGAACTATGC
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                            /(abb_nost="top-to")
/(clone lib="Xeropus laevis occyte"
/(clone lib="Xeropus laevis occyte")
//(clone lib="Xerop
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/clone="XENOPUS_SOURCE_ID:xlnoc001h24"
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/lab_host="Top-10 F'"
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                                                                                                                                         Score 110.8; DB 9; Pred. No. 1.4e-16; 0; Mismatches 47;
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170 Harbor Way, PO E
Tel: 650 837 7000
Fax: 650 837 8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 603)
Amundsen,C., Cachuela,N., Chen,F., Cheung,L.M., Chong,A., Murray,L., Oliva,J., Park,C., Reyes,J., Yungen,J. and Swimmer,C.
Expressed sequence tags from NCI_CGAP_ZEmb2, a Danio rerio embryonic library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: fchen@exelixis.com
DNA Sequencing by: Exelixis, Inc.
can be found through the I.M.A.G.!
http://image.llnl.gov
Plate: 14108 row: O column: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Danio rerio (zebrafish)
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Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:6521499"
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                                                                                                                                                                                                                                                                                                                 Score 110.2; DB 14;
Pred. No. 2.4e-16;
0; Mismatches 48;
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E. Consortium/LLNL at:
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Ostariophysi; Cypriniformes
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                                                                                                                                                                                                                                                                                                                                                                                 603;
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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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11256.701 Million cell updates/sec
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Gapop 60.0 , Gapext 60.0
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

REFERENCE AUTHORS. JOURNAL	SOURCE ORGANISM	RESULT 1 A91167 LOCUS DEFINITION ACCESSION VERSION		44.	4 4 3 3 2 1	c 40	ມ ພ 8 ວ	37	υ ω υ ω	3 G	32	30 31	29	27	9 U	24	22		a a 19			C 14		111	c 9		7 00	. UT .	ĿW		Result No. S
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EFINITION	•
CCESSION	A91167
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EYWORDS	
OURCE	Rattus sp.
ORGANISM	Rattus sp.
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
	Rattus.
EFERENCE	1 (bases 1 to 1491)
AUTHORS.	Icard-Liepkalns, C., Mallet, J. and Corresponding, N.A.
JOURNAL	Patent: WO 9827206-A 1 25-JUN-1998;

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Rattus sp.
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Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                      1 (bases 1 to 1491)
Liepkalns,C.I., Mallet,J. and Ravassard,P.
Polypeptide belonging to the family of basic helix-loop-helix
(bHLH) family and nucleic acid sequence corresponding thereto
Patent: JP 2001510464-A 1 31-JUL-2001;
RHONE POULENC RORER SA
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BD023626.1 GI:22564849
JP 2001510464-A/1.
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                           Rattus sp. (rat)
JP 2001510464-A/1
    31-JUL-2001
19-DEC-1997
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Best Local Similarity
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PI CHRISTINE ICARD LIEPKALMS, JACQUES MALLET, PHILIPPE RAVASSARD CO7K14/47, A61K31/711, A61K35/76, A61K38/00, A61K48/00, A61P25/00, Pt C12N15/09, A61K37/02
PC C12N15/00, A61K37/02
Strandedness: Single;
CC Topology: Linear:
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  GTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAGATCGAGACCCTGCGCTTCG
                             CCAACGACCGGGAGCGCAACCGCATGCACAACCTTAACTCCGCGCTGGATGCGCTGCGCG
                                                  CCAACGACCGGGAGCGCAACCGCATGCACAACCTTAACTCCGCGCTGGATGCGCTGCGCG
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/mol_type="genomic DNA"
/db_xref="taxon:10118"
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R.norvegicus mRNA for
Y10619
Y10619.1 GI:2072737
Direct Submission
Submitted (20-JAN-1997) P. Ravas
Hopital de la Pitie Salpetriere,
                                                                                                                            Ravassard,P., Chatail,F., Mallet,J. and Ica
Relax, a novel rat bHLH transcriptional reg
expressed in the ventricular proliferating
                                                                                                                                                                                                   Rattus norvegicus
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                            2 (bases 1 to Ravassard, P.
                                                                                                 central nervous system
J. Neurosci. Res. 48 (;
                                                                                                                                                                                                                                             Relax; transcriptional regulator Rattus norvegicus (Norway rat)
                                                                        9130143
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Sciurognathi; Muridae;
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  AAGTGCTCAGTTCCAATTCCAACCCCACCTAGCCCACTCTCGTACCGAGGGACTGCTCCG
                                                                                                                                                                                                                                                                CGCCCACCATCCAAGTGTCCCAAGAGAGACCCCAGCAACCCTTTCCCCGGAGCCTCGGACCACG
                                                                                                                                                                                                                                                                                                                                            ACTGTCACACCCCCCTTCCATTTTTTCCCAACCTCAGGATGGCGCCCTCATCCCTTGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                            TAGAAGAGGGGAGTGGGTGGGCGTACTCTAGTCCCGCGTGGAGTGACCTCTAAGTCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAAAACTTCGAAGCGAGCAGAGGGGTTCAGCTATCCACCGCTGCTTGACTCTGACCACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAAAACTTCGAAGCGAGCAGAGGGGGTTCAGCTATCCACCGCTGCTTGACTCTGACCACCC
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                                                                                                                     AAGCAGAAGCAGGTGACTGCCGAGGGACATCGAGGAAGCTCCGTGCGCGGCGCGGAGGGC
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/mol_type="mRNA"
/strain="Wistar"
/db_xref="taxon:101
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/product="relax"
/protein_id="CAA71630.1"
/protein_id="CAA71630.1"
/db_xref="GI:2072738"
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No. 0;
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                                                                                                                                                                                                                  AC127817
AC127817.3 GI:25077905
AC127817.3 HTGS
Muzny, D. Marie, Metzker, M. Lee., Abramzon, S., Adams, C., Al
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Ben
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
                                                                                                                                          Rattus norvegicus
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                           HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                     AC127817
Rattus norvegicus
                                                                                                                         Rattus.
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                                                                                                 (bases 1 to 258815)
                                                                                                                                                                                                                                                                                                       258815 bp DNA clone CH230-259G16, V
                                                                                                                                            Chordata;
Rodentia;
                                                                                                                                          Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                             WORKING
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ad, M., Benahmed, Brown, M.,

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Euteleostomi;
; Murinae;

HTG 19-NOV-2002 SEQUENCE, 3

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Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavacos, I., Ceasax, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Y., Chen, Z., Chu, J., Cheasa, J., Conter, A., Chen, Y., Chen, Y., Chen, Z., Chu, J., Cheasa, J., Chen, Y., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Jinh, H., Divya, K., Draper, H., Dugan, Rocha, S., Dunn, A., Dubin, K., Dival, B., Eaves, K., Egan, A., Bscotto, M., Eugen, C., Evans, C.A., Falls, T., Fan, G., Fernandez, G., Finley, M., Flagy, N., Forbes, L., Foster, M., Foster, M., Foster, M., Foster, M., Gebregoorgis, B., Geer, K., Gill, R., Grady, M., Guerra, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Haves, A., Hanil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Haves, A., Hanil, C., Hamilton, C., Hamilton, K., Hollins, B., Howells, S., Hladun, S. L., Hodgson, N., Hernandez, J., Harvey, Y., Havlak, P., Haves, A., Henderson, N., Hernandez, J., Harvey, Y., Liu, Y., London, P., Longacre, S., Lopez, J., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Kally, S., K
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:23912578. The sequence in this assembly is a combination of BAC based reads
contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                          and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separate by sized gaps filled with Ns to the estimated size. The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 258815)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                             may extend beyond the ends of the clone and there may be sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Worley, K.C.
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Center: Baylor College of Medicine
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FEATURES
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NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
GGACTGCTCCGAAGCAGAAGCAGGTGACTGCCGAGGGACATCGAGGAAGCTCCGTGCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             end_sequence:BZ169378"
59351 a 56888 c 58131 g 56821 t
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                                                                          TCCCTTGGATGCGCCCACCATCCAAGTGTCCCAAGAGACCCAGCAACCCTTTCCCCGGAGC
                                                                                                                                                                                                                                                                 CTAAGTCAGAGACTGTCACACCCCCCTTCCATTTTTTCCCAACCTCAGGATGGCGCCTCA
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                                                                                                                      TCCCTTGGATGCGCCCACCATCCAAGTGTCCCAAGAGACCCAGCAACCCTTTCCCGGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: GZXS

Center clone name: CH230-259G16

Center clone name: CH230-259G16

Center clone name: CH230-259G16

Center Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 224747 bases at least Q40

Consensus quality: 227951 bases at least Q30

Consensus quality: 229752 bases at least Q20

Estimated insert size: 228243; sum-of-contige estimation

Estimated insert size: 28243; sum-of-contige estimation
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/note="clone_boundary
clone_end:T7
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clone_end:Sp6"
complement(2865..3659)
/note="clone_boundary
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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0; Mismatches
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Sequence 7 f
AX698801
AX698801.1
                                                                       Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chorda
Wobus, A.M., St-Onge, L., Blyszczuk, P. and Hoffmann, U. A method for differentiating stem cells into insulin-producing
                                                        Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCGCTTTCTCCAGAGTGACCTAATCCAGTGT
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                                                      ; Metazoa;
Eutheria;
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from Patent WO02086107
                                                                                                                                                GI:29499589
                                                      Chordata;
Rodentia;
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Sciurognathi; Muridae
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Patent: WO 02086107-A 7 31-OCT-2002;
Patent: WO 02086107-A 7 31-OCT-2002;
DeveloGen Aktiengesellschaft fuer Entwicklungsbiologische Forschung
(DE) ; INSTITUT FUER PFLANZENGENETIK UND KULTURPFLANZENFORSCHUNG
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Sommer, L., Ma,Q. and Anderson, v.v. .

Direct Submission
Submitted (24-OCT-1996) Biology 216-76, California Institute of Submitted (24-OCT-1996) Biology 216-76, California Institute, Pasadena, CA 91125,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 861)
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U76208
                                                                                                                                                                                                                                                                                                                                                                                  neurogenins, a novel family of atonal-related bHLH transcription factors, are putative mammalian neuronal determination genes that reveal progenitor cell heterogeneity in the developing CNS and PM Mol. Cell. Neurosci. 8 (4), 221-241 (1996)
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LDALRGYLFTFPDDAKLTKLETLRFAHNYIWALTQTLRIADHSFYGEPSPVPCGELGS
PGGGSNGDWGSIYSPVSQAGNLSPTASLEEFPGLQVPSSPSYLLPGALVFSDFL"
274 c 250 g 155 t
                  /gene="ngn3"
/function="bHLH t
/note="NGN3"
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160. .804
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Best Local
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Submitted (26-MAR-2001) Hormone Research Institute, University California San Francisco, 513 Parnassus Ave, HSW1090, San Francisco, CA 94145-0534, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92;
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Mus musculus neurogenin
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Schwitzgebel, V. and German, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Regulation of the pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and German, M.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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pGGGSNODWGSIYSPVSQAGNLSPTASLEEFPGLQVPSSPSYLLPGALVFSDFL"

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|mol_type="genomic DNA"
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On (
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Direct Submission
Direct Submission
Submitted (04-NOV-1996) G.J. Gradwohl, IGBMC,
CNRS-INSERM-Universite Louis Pasteur, BP163, C.U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (01-AUG-2000) Lemaigre F.P., Hormone and Metabolic Research Unit, Louvain University Medical School, Avenue Hipp 75, box 7529, Brussels 1200, BELGIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jacquemin, P., Durviaux, S.M., Jensen, J., Godfraind, C., Gradwohl, G., Guillemot, F., Madsen, O.D., Carmeliet, P., Dewerchin, M., Collen, D., Rousseau, G.G. and Lemaigre, F.P.
Transcription factor hepatocyte nuclear factor 6 regulates
pancreatic endocrine cell differentiation and controls expression
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4 (bases 1 to 5567)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                                                        /gene="MATH4B"
4145. .4151
                                                                                                                                                                                                                                                                                     /cell_type="embryonic stem cells"
/clone_lib="Genomic library No.62,
cloned_in BamHI"
/codon_start=1
/product="neurogenin 3"
/protein_id="CAA70366.1"
/db_xref="GI:1666088"
                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="SV129"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , 2000 this sequence version replaced gi:1666087
Location/Qualifiers
                                                                                       note="putative"
1923. .5567
                                                                                                                           'gene="MATH4B"
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1145. .5567
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Matches 92; Conser
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                                                                                                                                                                                                                                                                                                                                                                         Contact: mccombie@cshl.org
Project
Project name: RP23-121F10
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McCombie,W R., Baker,J.P., Balija,V., Dedhia,N.N., de la
Bastide,M., Katzenberger,F., Kuit,K., King,L., Kirchoff,K.A.,
Miller,B., Muller,S., Nascimento,L.U., O'Shaughnessy,A.L.,
Prescon,R.R., Santos,L., Spiegel,L.A., Palmer,L., Yang,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC109783.1 GI:18581594
HTG: HTGS_DHASE1; HTGS_DRAFT.
Mus muscullus (house mouse)
Mus musculus
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                                                                                                                                                                                                                                                                    Insert size: 173000; agarose-fp
Insert size: 141616; sum-of-contigs
Quality coverage: 4.00 in Q20 bases; agarose-fp
Quality coverage: 3.70 in Q20 bases; sum-of-contigs
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AC109783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (07-FEB-2002) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                      Clone name: RP23-121F10
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                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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/translation="MAPHPLDALTIQVSETOOPFPGASDHEVLSSNSTPPSPTLIPR

DCSEAFUDCTSTRILARRGGRNRFKSELALSKQRRSRRKKANDRERNRMHNLNSA

LDALRGYLPTFPDDAKLTKIETLRFAHNYIWALTQTLRLADHSFYGPEPFVFCGELGS

PGGGSNGDWGSIYSPVSQAGNLSPTASLEEFPGLQVPSSPSYLLPGALVFSDFL"
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17785: contig of 17785 bp in length 17874: gap of unknown length 30356: contig of 12482 bp in length 30444: gap of unknown length
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                           2 (bases 1 to 215050)
McPherson, J.D. and Waterston, R.H.
Direct Submission
                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 215050)
McPherson,J.D. and Waterston,R.H.
The sequence of Mus musculus clone
                                                            The sequence of Mus musculus Unpublished
                                                                                                                                                                                                Mus musculus chromosome UNK clone RP23-459M2, WORKING
Parkway, St. Louis, MO (bases 1 to 215050)
                   Submitted (15-JUL-2002)
                                                                                                                                Mus musculus
                                                                                                                                        HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP Mus musculus (house mouse)
                                                                                                                                                               AC127417.2 GI:24137619
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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TITLE
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Consensus quality: 212279 bases at least Q40
Consensus quality: 213137 bases at least Q30
Consensus quality: 213137 bases at least Q30
Consensus quality: 213590 bases at least Q20
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On Oct 19, 2002 this sequence version replaced gi:21759524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Washington University Genome Sequencing Center Center code: WUGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality coverage: 11.89 in Q20 bases; agarose-fp Quality coverage: 10.54 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: plasmid; 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: M13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: M_BA0459M02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: submissions@watson.wustl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert size: 192000; agarose-fp
Insert size: 217944; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                                                                                                                                                                                 /note="assembly_name:Contig33"
27419. .49797
                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type= 5000:10090"
/db_xref="taxon:10090"
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                                                                      /note="assembly_name:Contig36"
132696. .215050
                                                                                                                                   /note="assembly_name:Contig35"
                                                                                                                                                                                   /note="assembly_name:Contig34"
                                                                                                                                                                                                                                                                                   /note="assembly_name:Contig32"
                                                                                                                                                                                                                                                                                                                                   'note="assembly_name:Contig31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                        clone="RP23-459M2"
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27418: gap of unknown length
49797: contig of 22379 bp in length
49897: gap of unknown length
79378: contig of 29481 bp in length
79478: gap of unknown length
79478: gap of unknown length
132595: contig of 53117 bp in length
132695: gap of unknown length
215050: contig of 82355 bp in length.
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16689:
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4327: gap of unknown length
6589: contig of 12262 bp in length
6689: gap of unknown length
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                    embly_name:Contig37"
52885 g 53012 t
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REMARK
COMMENT
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AUTHORS
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Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length
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web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.(
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.)
                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramur.
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BC036847
Homo sapiens neurogenin 2, mRNA
IMAGE:5247719), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (23-AUG-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A.
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                             Gaithersburg, Maryland;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
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9.5e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens neurogenin
AF303002
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                                                                                                            Submitted (06-SEP-2000) Center for Basic Neuroscience - I Southwestern Medical Center, 5323 Harry Hines Boulevard,
                                                                                                                                                                                                                                       Simmons, A.D., Horton, S., Abney, A.L. and Johnson, J.E. Neurogenin2 expression in ventral and dorsal spinal progenitor cells is regulated by distinct enhancers Dev. Biol. 229 (2), 327-339 (2001)
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
                                                                                                                                                   Direct Submission
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Simmons, A.D., Horton, S.,
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protein_id="AAH46847.1"
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INALTETLRLADHCGGGGGGLDGALFSBAVLLSPGGASAALSSSGDSPSPASTWSCTN
/organism;"Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="synonyms: Atoh4, Math4A, /db_xref="LocusID:63973"
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Homo sapiens BAC clone RP11-402J6
AC023886
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           Submitted (18-FEB-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                  3 (bases 1 to 179697)
Waterston, R.H.
                                                                                              Radionenko, M. and Abbott, A. The sequence of Homo sapiens
                                                                                                                                                                      Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                               Mammalia; Eutheria; Primates; Catarrhini; 1 (bases 1 to 179697) Sulston, J.E. and Waterston, R.
                                                                                                                                                                                                                                                          Homo sapiens
          University School of Medicine,
                                      Direct Submission
                                                                                Unpublished (2001)
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GALFSEAVLLSPGGASAALSSSGDSPSASTWSCTNSPAPSSSVSSNSTSPYSCTLSP
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/o // // // // // // // // // // // // /	SOURCE INFORMATION: The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org VECTOR: pBACe3.6 NEIGHBORING SEQUENCE INFORMATION: The clone sequenced to the right is AC004049, 2000 bp overlap; the clone sequenced to the right is RP11-148B6. Actual end of this Location/Qualifiers 1. 179697	NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions. This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest. MAPPING INFORMATION: Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc	Waterston, R.H. Direct Submission Submitted (15-MAR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 5 (bases 1 to 179697) Waterston, R. Direct Submission Submitted (20-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Mar 15, 2002 this sequence version replaced gi:17352441.
repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region	repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region	repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region	
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                                                                                                                                                                                                                                                                                  The human neurogenin 3 homolog maps to chromosome 10q21.3 and its expression pattern is identical to that of its murine counterparts unpublished
                                                                                                                                                                                                       Submitted (16-MAR-1999) Ravassard P., Lgn, CNRS UMRC 9923, Hopital de la Pitie Salpetriere, Bat. CERVI, 83 Bd. de l'Hopital, 75013
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Ravassard, P.
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bHLH transcription factor; neurogenesis; neurogenin 3; ngn3 gene.
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AJ133776
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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tive 0; Mismatches 0;
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Search co completed: January 29, 2004, 21:29:57 ne : 5314 secs

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Result
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US-08-722-570-23
US-08-910-973-21
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US-09-354-243B-25
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US-09-551-974A-75	US-09-022-765-75	US-09-183-861-75	US-08-434-877-1	US-08-086-439C-1	US-09-252-991A-9532	US-09-252-991A-1904	US-09-252-991A-14810	US-09-252-991A-9635	US-08-925-171-5	US-08-751-782-5	US-09-252-991A-9622	US-09-687-731-10	US-09-687-731-8	US-09-687-731-2	US-09-552-733-6	US-08-465-712C-6	US-08-358-627F-6
Sequence 75, Appl	Sequence 75, Appl	Sequence 75, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 9532, Ap	Sequence 1904, Ap	Sequence 14810, A	Sequence 9635, Ap	Sequence 5, Appli	Sequence 5, Appli	Sequence 9622, Ap	Sequence 10, Appl	Sequence 8, Appli	Sequence 2, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli

ALIGNMENTS

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RESULT 1
US-08-932-411A-19
US-08-932-411A-19
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COMPUTER: IBM PC COMPARTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Vers
SOFTWARE: PATENTIN Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932,411A
FILING DATE: 15-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/772,009
FILING DATE: 19-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/722,570
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Silva, Robin M.
REGISTION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A--
TELECOMMUNICATION INFORMATION:
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ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ma, Qiufu
TITLE OF INVENTION: NEUROGENIN
NUMBER OF SEQUENCES: 31
                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 804 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                 FEATURE:
                                     NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNECC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                         TOPOLOGY:
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CITY: San Francisco
                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP STREET: Four Embarcadero Center, Suite 3400
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                                                                                                                                                                                                                                                                                                                                                                                                                                               19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A-63902-3/RFT/RMS
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                                                                                                         US-08-932-411A-13
                                                                                                                           RESULT 3
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                                                 Sequence 13, Application US/08932411A Patent No. 6566496 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13,
Patent No. 6
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Best Local
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 398-324
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/722,570 FILING DATE: 27-SEP-196 CLASSIFICATION: 5365
APPLICANT: Anderson, David J. APPLICANT: Ma, Qiufu TITLE OF INVENTION: NEUROGENI
                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 738 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-63902/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Anderson, APPLICANT: Ma, Qiufu TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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                                                                                                                                                                               304 GAGCGCAACCGCATGCACAACCT 326
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                                                                                                                                                                                                                                                                      Similarity
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llarity 100.0%; Pred. No. 9.9e-37;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                             unknown
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                                                                                                                                                                                                                                                                    Score 23; DB 4; Length 738; Pred. No. 0.072;
                                                                                                                                                                                                                                                      Mismatches
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RESULT 4
US-08-910-973-21
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Best Local S
Matches 23
                                                                                                                                                                      Sequence 21, Application US/08910973
Patent No. 5795723
GENERAL INFORMATION:
APPLICANT: Tapscott, Stephen J.
APPLICANT: Olson, James M.
TITLE OF INVENTION: Expression of Neurogenic bHLH Genes in Primitive Neuroectoder NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen O'Connor Johnson KindnessPLLC
STREET: 1420 Fifth Avenue, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 398-32-
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
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ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-63
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                      ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATER: PATEN: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
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PRIOR APPLICATION DATA:
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ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP
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CLASSIFICATION:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                  COUNTRY: USA
ZIP: 98101-2347
                                                                                                                                        STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/772,009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 GAGCGCAACCGCATGCACAACCT 326
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94111-4187
                                                                                                                                                          Seattle
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. 0.072;
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CURRENT APPLICATION DATA:

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RESULT 5
US-09-499-227-21
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Sequence 21, App.-
Sequence 21, App.-
No. 6444463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 206-225-0779
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PM PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:

NAME: Sheiness, Diana K.
REGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: FHCR-1-10958
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-682-8100; 206-224-0735 (direct)
TELEPAX: 206-225-0779
                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen O'Connor Johnson KindnessPLLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 08-MAY-1995 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 1
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APPLICATION NUMBER: US 08/239,238
FILING DATE: 06-MAY-1994
                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Tapscott, Steph
APPLICANT: Olson, James M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OLECULE TYPE:
PRIOR APPLICATION DATA
                 APPLICATION NUMBER: US 08/239,238 FILING DATE: 06-May-1994
                                                                     APPLICATION NUMBER: US/09/4 FILING DATE: 05-August-1998
                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 98101-2347
                                                                                                                                                                                                                                                                         STREET: 1420 P
CITY: Seattle
                                                                                                                                                                                                                                                              STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                      EXPRESSION OF INVENTION: Expression of Neurogenic bHLH Genes in Primitive Neuroectoder
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                                                                                                                                                                                                                                                                                            1420 Fifth Avenue, Suite 2800
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                                                                                                                                                                                                                                                                                                                                                                                                          Stephen J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.6%; Score 23;
100.0%; Pred. No.
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                                                                                        US/09/499,227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6566496
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 206-225-0779
INFORMATION FOR SEQ ID NO:
                                                                                                                                           SOFTWARE: PatentIn Release #1.0, VICURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932,411A
                                              FILING DATE: 19-DEC-PRIOR APPLICATION DATA:
                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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LENGTH: 1333 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/9: FILING DATE: 07-August-1997 ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
FILING DATE: 30-Octo
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 1
FILING DATE: 08-May-
PRIOR APPLICATION DATA:
                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP
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IMMEDIATE SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
ATTORNEY/AGENT INFORMATION
             APPLICATION NUMBER: FILING DATE: 19-DEC
                                                                                                                                                                                                                                                                                                 CITY: San Francisco
STATE: California
                                                               APPLICATION NUMBER: US 08/772,009 FILING DATE: 19-DEC-1996
                                                                                                                FILING DATE: 1
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OCATION:
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                 19-DEC-1996
                                                                                                                               15-SEP-1997
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100.0%; Pre
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                                US 08/722,570
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ER: FHCR-1-12742
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Pred. No.
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                                                                                                                                                                                   Version #1.30
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0.072;
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REFERENCE/DOCKET NUMBER: A-TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989 TELEFAX: (415) 398-3249

REGISTRATION NUMBER:

38,304

A-63902-3/RFT/RMS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 398-324.
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                         APPLICATION NUMBER: US 08/
FILING DATE: 06-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT
FILING DATE: 08-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                          TELEFAX: 206-225-0709
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 98101-2347

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
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APPLICANT: Hollenberg, Stanley M.
                                                                                                                              REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: FHCR-1-8933
TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 02-NOV-1995 CLASSIFICATION: 514
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Christensen O'Connor Johnson KindnessPLLC STREET: 1420 Fifth Avenue, Suite 2800
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TOPOLOGY: un
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Seattle
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                                     ENGTH:
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                                                                                                                                                                                         Broderick, Thomas F
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310 base pairs nucleic acid
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Tapscott, Stephen J.
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                                                                                                                206-682-8100
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                                                                                                                                                                                                                                                                                                         US 08/239,238
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Patent No. 5/>3/-.
Thirdal INFORMATION:
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Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                           FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/239,238
ETILING DATE: 06-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: WO PCT/US95/05741
FILING DATE: 08-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION UMBER: PCT/US96/17532
PRICH APPLICATION DATA:
APPLICATION UMBER: BCT/US96/17532
APPLICATION UMBER: 30-October-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sheiness, Diana K.
REGISTRATION NUMBER: 35,356
REGISTRATION NUMBER: FICR-1-10958
                                                                                                                                                                                       TELEFAX: 206-225-0779 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,973
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ORIGINAL SOURCE:
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                                                        MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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IMMEDIATE SOURCE:
CLONE: 20A1 (neuroD3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION: 1...
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                                        ORGANISM:
                                                                                                TOPOLOGY:
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                                                                                                                                                    LENGTH:
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                                                                                                                                 : 1268 base pairs nucleic acid
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                                      Homo sapiens
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                                                                                        linear
                                                                                                                                                                                                                        206-682-8100; 206-224-0735 (direct)
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                                                                           DNA (genomic)
                                                                                                                double
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0; Mismatches
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US-09-499-227-12
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 Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                     TELEFAX: 206-225-0779
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                           MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 206-682-8100; 206-224-0735 (direct)
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/910,973 FILING DATE: 07-August-1997 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 1
FILING DATE: 30-Octob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 06-May-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US95/05741
FILING DATE: 08-May-1995
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PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/499,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tapscott, Stephen J. APPLICANT: Olson, James M. TITLE OF INVENTION: Expression
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                                                                                                            IMMEDIATE SOURCE:
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LOCATION:
                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 35,356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                                                        STRANDEDNESS:
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                                                                                                                              RGANISM:
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                                                                                                                                                                                                    nucleic acid
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                                                                                              20A1 (neuroD3)
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55..768
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 Score 21;
 DB 4;
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0.74;
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Length 1268;
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US-08-552-142A-10
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Matches 21; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Weintraub, Harold APPLICANT: Lee, Jacqueline E. APPLICANT: Tapscott, Stephen
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                                                                                                          NAME/KEY:
LOCATION:
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                                             Local
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                                                                                                                                                                                         ORGANISM:
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729 CGGGAGCGCAACCGCATGCAC 749
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                               Similarity 21; Conser
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                                                                                                                                                                                                                                                                    nucleic acid
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Hollenberg, Stanley M.
WINTION: Neurogenic Differentiation (NeuroD) Genes
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55..1194
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                                            1.4%; Score 21;
100.0%; Pred. No.
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                               Mismatches
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                                             DB 1;
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CGGGAGCGCAACCGCATGCAC 459

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RESULT 11
US-08-910-973-10
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                                                                US-09-499-227-10
                                                                               RESULT 12
           Sequence 10, Applicat Patent No. 6444463
GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: WO PCT/US9
FILING DATE: 08-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: PCT/US96/1
FILING DATE: 30-October-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1535 base pair
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-682-8100; 206-224-0735 (direct)
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PRIOR APPLICATION NUMBER: US 08/239,238
APPLICATION NUMBER: US 08/239,238
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Olson, James M.
TITLE OF INVENTION: Expres
                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY:
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Sheiness, Diana REGISTRATION NUMBER: (
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                                                                                                                                                                                                               Local
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                                                                                                                                                            729 CGGGAGCGCAACCGCATGCAC 749
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                                               Application US/09499227
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Tapscott,
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Stephen J
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Pred. No.
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0.74;
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RESULT 13
US-09-234-332-3
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                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                          Query Match
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FILING DATE: 08-May-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/17532
FILING DATE: 30-October-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
US 08/910,973
FILING DATE: 07-August-1997
                                                  APPLICANT: Cedars-Sinai Medical Center APPLICANT: Michel F. Levesque, M.D. APPLICANT: Toomas Neuman, Ph.D.
                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 206-225-0779
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: Expression of Neurogenic bHLH Genes in Primitive Neuroectoder NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
ATTORNEY AGENT INFORMATION:
NAME: Sheiness, Diana K.
REGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: FH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/4
FILING DATE: 05-August-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo
IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 206-682-8100; 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 131
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/239,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLONE: 14B1 (neuroD2)
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                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
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                                                                                                                                                                                                                                       439
                                                                                                                                                                                                                                                                     729 CGGGAGCGCAACCGCATGCAC 749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                double
CONVERSION OF NON-NEURONAL CELLS INTO NEURONS; TRANSDIFFERENTIATION OF EPIDERMAL CELLS 41494
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                                                                                                                                                                                                                                                                                                                                           1.4%;
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; Pred. No.
                                                                                                                                                                                                                                       459
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FILE REFERENCE:

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US-08-358-627F-4/c
; Sequence 4, Application US/08358627F
; Patent No. 6177242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: U.C.
COUNTRY: U.S.A.
COUNTRY: U.S.A.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
CO
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Best Local Similarity
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
                                                                                                                                                                                                           TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/234,332A CURRENT FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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ORGANISM: Human
FEATURE:
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LOCATION: (1219)...(1226)
OTHER INFORMATION: n at 1219 and 1226; n
STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
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LOCATION: (0)...(0)
OTHER INFORMATION: Neurogenic basic-helix-loop-helix protein (Neuro
OTHER INFORMATION: D2) gene Genbank Accession U58681
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TITLE OF IN
TITLE OF IN
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FILING DATE: 14-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 25
REFERENCE/DOCKET NUMBER:
                                                                             LENGTH: 50 L-
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Meyers,
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                                                                                                                                            50 base pairs
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                                          linear
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                                                                      single
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100.0%;
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Regulatory and Coding Sequences For The B2-Subunit of the
Neuronal Nicotinic Acetylcholine Receptor and Transgenic
Animals Made Using These Fragments or Mutated Fragments
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0.74;
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; Sequence 11, Application US/08793044
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                                                                                                                            US-08-793-044-11
                                                              Matches
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Best Local Similarity
                                                                                           Query Match
                                                                                                                                                                                                                   TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: ST
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FR 9-
FILING DATE: 16-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cervini, Riccardo
APPLICANT: Mallet, Jacques
TITLE OF INVENTION: NOVEL VESICULAR ACETYLCHOLINE CARRIER
                                                                                                                                           MOLECULE TYPE: other nucleic acid
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                                                                            Local
                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: WO PCT/FR95/01073 FILING DATE: 10-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 500 Arcola CITY: Collegeville
                                                                                                                                                                                                                                                                                                                  NAME: Savitzky Esq., Martin F. REGISTRATION NUMBER: 29,699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U
ZIP: 19426
                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Rhone-Poulenc Rorer Inc. STREET: 500 Arcola Road, Mailstop 3C43
                                                                                                                                                                                                          ENGTH:
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                                                                            Similarity
                             GCAGGTAGCGAGAGGAGCA 19
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GCAGGTAGCGAGGAGCA 15
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                                                                                                                                                                                                        50 base pairs
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                                                              Conservative
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                                                                                                                                                          linear
                                                                                                                                                                                                                                                                       (010)
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100.0%; Pred. No. 7.2
ative 0; Mismatches
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Sylvie
                                                                          1.3%; Score 19;
100.0%; Pred. No.
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                                                              Mismatches
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Oligonucleotide fo	Novel murine polyn	Human immune/haema	Human immune/haema	_	Human reproductive	Human neurogenin 1	Human NeuroD2 gene	Human bHLH family	DNA encoding human	Human neurogenic d	Human bHLH family	DNA encoding human	Human neurogenic d	Human neurogenin 1		Human RT-PCR upstr	Mouse atonal homol	Mouse atonal homol	Mouse neurogenin 2	œ		Mouse neurogenic d	Mouse bHLH family	DNA encoding murin	Chicken atonal hom	Murine neurogenin-	Mouse neurogenin 1	PCR primer used to	Human Neurogenin-3	Human cDNA encodin	Human neurogenin 3		Human neurogenin 2	Mouse spliced tran	Rat spliced transc

ALIGNMENTS

PN W09827206-A2. XX PD 25-UUN-1998. XX XX XX XX PF 19-DEC-1997; XX			2	<<	FT			FH Key	X	OS Rattus sp.						DT 05-OCT-1998	XX	AC AAV42512;	X		AAV42512	RESULT 1
997; 97WO-FR02368.		998.	6-A2.		/product= RELAX	/*tag= a	4591103	Location/Qualifiers		•	system disorder; ss.	<pre>protein expression; central nervous system; CNS; treatment;</pre>	control; gene expression; transcriptional activator; targeting;	Basic helix-loop-helix; BHLH; RELAX; Rat Embryonic Longitudinal	cDNA encoding a novel BHLH protein designated RELAX.	998 (first entry)				AAV42512 standard; cDNA; 1491 BP.		
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                                                                                                                            neurogenesis
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  Location/Qualifiers
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                                                                                                                                                   vector;
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27-SEP-1996;
12-NOV-1996;
                                                WO200009676-A2
                                                                                                                                                                                                                                                                    cerebroprotective;
                                                                                                                                                                                                                                                                                                             Neurogenin-3; NGN-3; non-neuronal cell; NNC; neurogenesis;
Phox2a protein; neuronal subtype-specific marker; growth factor;
neural differentiation; transplantation; neuronal dysfunction;
optical nerve damage; auditory nerve damage, neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine neurogenin-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ51981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ51981 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in the present invention. The neurogenin nucleic acids can be in a host cell, transformed using an expression vector, to proceed the proteins and the antibodies raised recombinant proteins. The proteins and the antibodies raised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Mouse neurogenin 3 is one of several neurogenin proteins discussed in the present invention. The neurogenin nucleic acids can be express
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 9; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse
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                                                                                                                                                                                                                                                                                              neuroprotective; nootropic; anticonvulsant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteins. The proteins and the antibodic are useful in the study of neurogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
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96US-0722570.
96US-0030864.
96US-0772009.
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                                                                                                                                             Location/Qualifiers
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                                                                                                  product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful in neurogenesis -
derived from rat and Xeno
                                                                                                                                                                                                                                                                  immunesuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                       (NGN3) nucleic acid sequence.
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                                                                                             "Murine neurogenin-3 protein"
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9e-35;
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24-FEB-2000.

01-JUN-2000; 2000WO-US15410.

Mus musculus.

transgenic

animal;

88

WO200073764-A2

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Matches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modulate neural differentiation or as sources of recombinantly produced neurogenins and phox2a proteins for use in transplantation. The cells also have a variety of in vivo uses, e.g. for transplantation at sites of neuronal dysfunction e.g. patients with hearing or vision loss due to optical or auditory nerve damage, brain or spinal cord injuries, and neurodegenerative disorders e.g. Alzheimer's disease. The present sequence encodes murine neurogenin-3 (NGN-3), a transcription factor. NNCs differentiate into neurons through the recombinant expression of a transcription factor that induces a core program of neurogenesis. Forced expression of murine NGN3 can elicit expression of at least some neuronal phenotypic markers even in NNCs.
                                                                                                                                hearing impairment; vestibular effect; balance disorder; osteoar cellular proliferation; cerebellar granule neuron; gene therapy; mechanoreceptive cell growth; auditory; osteopathic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The patent discloses a method for inducing non-neuronal cells (NNC) to differentiate into neurons and for NNCs to express a neuronal subtype specific marker. Transformed host cells are used as sources of neuron and other growth factors; in culture for screening compounds that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inducing non-neuronal cells to differentiate into neurons and for non-neuronal cells to express a neuronal subtype-specific marker, comprising contacting the non-neuronal cells with a vector containing neurogenin nucleic acid -
                                                                                                                                                                                                               Mouse neurogenin 3 (ngn3) cDNA,
                                                                                                                                                                                                                                                24-APR-2001
                                                                                                                                                                                                                                                                                                            AAF27266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1;
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                                                                                                                                                                                  homologue; orthologue; atonal-associated protein; deafness;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCGCTGGATGCGCTGCGCGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAG
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                                                                                                                                                                                                                                                                                                            standard; cDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                804 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.3%;
                                                                                                                                                                                                                                                                                                            861
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Pred. No.
                                                                                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                 SEQ ID NO:24.
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9e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 804;
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                                                                                                                                                                     osteoarthritis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid sequence, or any of its homologues or orthologues as therapeutic agents for the treatment of deafness, partial hearing loss, cestibular effects due to damage or loss of inner hair cells, costeoarthritis and abnormal cell proliferation. The invention also encompasses methods of screening for compounds which affect the expression of an atonal -associated nucleic acid sequence in an animal, and transgenic animal in which an allele of a native atonal-associated gene is replaced by a heterologous nucleic acid sequence, thus inactivating the atonal-associated allele. The nucleic acids or proteins may be used in a method of treating an animal for hearing impairment, joint disease, balance disorders, abnormal cell proliferation, or other disease related to loss of a functional atonal-associated nucleic acid or protein. They may particularly be used to treat an animal with a cofficiency in cerebellar granule neurons or their precursors, and may also be used in promoting mechanoreceptive cell growth and generating hair cells. The present sequence represents an atonal-associated nucleic acid sequence referred to in the invention.

Note: The present sequence is not shown in the specification, but
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Best Local
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                                                                                                                           glucose intolerance; antidiabetic;
                                                                                                                                      Mouse; transcription factor; neurogenin 3; ngn3; stem cell; differentiation; beta-cell; insulin; diabetes; hyperglycaemia;
                                                                                                                                                                                              Mouse transcription
                                                                                                                                                                                                                                 11-FEB-2003
                                                                                                                                                                                                                                                                      ABV75970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 osteoarthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Therapeutic use of atonal-associated nucleic acids or amino acids, or any of its homologs or orthologs, for the treatment of e.g. deafness,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zoghbi HY, Bellen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1999;
19-JAN-2000;
                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                        ABV75970 standard; cDNA; 861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-032190/04
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCGAGACCCTGCGCTTCGCCCACAACTACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCGCTGGATGCGCTGCGCGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                861 BP;
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2000US-0176993.
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              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                              factor neurogenin 3 cDNA.
                                                                                                                                                                                                                                 entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Birmingham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           o the use of atonal-associated nucleic as any of its homologues or orthologues as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                274 C; 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 92; DB; Pred. No. 9e-
0; Mismatches
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9e-35;
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27-JAN-2003 (first entry)

821 522

Murine neurogenin 3 (Ngn3) gene

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                  animals or human for treatment of pancreatic diseases, metabolic syndrome and metabolic disorders with impaired glucose levels such as diabetes, hyperglycaemia and impaired glucose tolerance (claimed). The cells can also be used to identify compounds which stimulate beta-cell differentiation, insulin secretion or glucose responsiveness. Differentiated beta-cells can be used to study the toxic and other effects of exogenous compounds on beta-cell function. In an example from the invention, Pax6 cDNA was inserted into expression vector pACCMV.pLpA under the control of the cytomegalovirus promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a gene which is required for the specification of the early endocrine precursor in the pancreatic epithelium and which is down-regulated once endocrine differentiation begins. The invention provides a claimed method for differentiating stem cells (especially embryonic, adult or somatic stem cells and primordial germ cells) into insulin-producing cells. This involves culturing stem cells in a suitable medium and activating at least one gene involved in beta-cell differentiation. Preferred genes including Pdx1, Pax4, Pax6 and ngn3 (see ABV15967-70). Gene activation comprises the delivery of the gene into stem cells using a viral delivery system, or the delivery of a protein product of the gene into stem cells. The insulin-producing cells can be transplanted into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of cDNA encoding the murine basic helix-loop-helix transcription factor neurogenin 3 (n a gene which is required for the specification of the early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Differentiating stem cells into insulin-producing cells useful for treating pancreatic diseases, by culturing stem cells in suitable medium and activating gene involved in beta-cell differentiation -
                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 58-59; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-075629/07.
  AAD46872 standard; DNA; 1860 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-APR-2001; 2001US-284531P.
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                                                                                                                                                                                                                                                              92;
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                                                                                                                                             ATCGAGACCCTGCGCTTCGCCCACAACTACAT 853
                                                                                                                                                                                                                         GCGCTGGATGCGCTGCGCGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAG
                                                                                                                                                                                                                                                                                                                                                 861 BP; 182 A; 274 C; 250 G; 155 T; 0 other;
                                                                                                                                                                                     GCGCTGGATGCGCTGCGCGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activating gene involved in beta-cell differentiation
                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "Mouse ngn3"
                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                           6.3%;
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Pred. No.
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                                                                                                                                                                         AAC61090 standard; DNA; 1861
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1860 BP; 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                for treating type 2 diabetes mellitus and for replacing beta cells lost to autoimmune destruction in individuals with type 1 diabetes. The method is useful in cell therapy. The present sequence is murine neurogenin 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method for producing a mammalian islet cell. The method comprising introducing into a mammalian cell a nucleic acid molecule encoding an islet transcription factor for expression of the islet transcription factor for production of islet cell phenotype in the cell. The islet transcription factor is a neuroendocrine basic helix-loop-helix (bHLH) transcription factor. The method is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Page 89-90; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Producing a mammalian islet cell for treating diabetes mellitus comprises introducing into a mammalian cell a nucleic acid molecule encoding neuroendocrine basic helix-loop-helix transcription factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcription factor; neuroendocrine basic helix-loop-helix; bHLH; type 2 diabetes mellitus; autoimmune destruction; type 1 diabetes; islet cell; cell therapy; neurogenin 3; Ngn3; murine; gene; ds.
                Mus musculus
                                                       Neurogenin
                                                                                      Murine neurogenin 3 (Ngn3) genomic DNA sequence
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                                                                                                                                                                                                                                                                                                                                      762
                                          cell precursor
                                                                                                                                                                                                                                                                                                                                                                 92;
                                                                                                                                                                                                                                                                            ATCGAGACCCTGCGCTTCGCCCACAACTACAT 853
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                                                         3; Ngn3; cellular differentiation; diabetes mellitus;
                                                                                                                                                                                                                                                                                                                                                               6.3%;
ilarity 100.0%;
Conservative
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                                                                                                                  entry)
                                           identification;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         537 G;
                                                                                                                                                                                                                                                                                                                                                                                                                         367 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                             DB 24; I
8.7e-35;
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                                                                                                                                                                                                                                                                                                                                                                                            Length 1860;
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RESULT 8
AAF27254
ID AAF2
XX
AC AAF2
XX
AC AAF2
XX
DT 24-A
XX
DE MOUS
XX
KW Aton
KW hear
KW cells
KW mech
KW tran
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The human neurogenin 3 Ngn3 DNA sequence AAC61089 encodes the Ngn3 CC protein AAY85617. The Ngn3 gene is located at chromosome position 10q22.1-22.2. The invention relates to the human Ngn3 nucleotide and protein sequences, and includes an antibody recognising the Ngn3 protein. Also included in the invention is a method for identifying an islet cell precursor, the method involves analysing a cell for the expression of the Ngn3 gene product, where detection of the product is indicative of an C Ngn3 gene product. The Ngn3 DNA sequence is useful as a diagnostic reagent for detecting (in a subject) a predisposition to a defect in pancreatic islet cell function or formation associated with a defect in Ngn3 activity. The Ngn3 protein is useful for identifying beta-cell C precursor cells expressing Ngn3, and to alter cellular differentiation in culture in vivo to produce new beta-cells to treat patients with diabetes mellitus. The present sequence represents the murine Ngn3 genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 92; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cbs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human neurogenin 3 polypeptides and polynucleotides encoding them, useful for diagnosis, prevention and treatment of diabetes mellitus and to identify individuals at risk of diabetes -
               Atonal; homologue; orthologue; atonal-associated protein; deafness; hearing impairment; vestibular effect; balance disorder; osteoarthritis; cellular proliferation; cerebellar granule neuron; gene therapy; mechanoreceptive cell growth; auditory; osteopathic; cytostatic;
                                                                                                                                                                                                  AAF27254 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1861 BP; 397 A; 560 C; 537 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 18; Page 49-50; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAY85618.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200059936-A1
                                                                                                Mouse atonal homologue 5 (ATOH5,
                                                                                                                                  24-APR-2001
                                                                                                                                                                 AAF27254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
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                                                                                                                                                                                                                                                                                   1456
                                                                                                                                                                                                                                                                                                                                                                           GCGCTGGATGCGCTGCGCGGTGTCCTGCCCAACCTTCCCGGATGACGCCAAACTTACAAAG
                                                                                                                                                                                                                                                                                                                  ATCGAGACCCTGCGCTTCGCCCACAACTACAT 853
                                                                                                                                                                                                                                                                                   ATCGAGACCCTGCGCTTCGCCCACACTACAT 1487
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product= "Ngn3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "Neurogenin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *tag=
                                                                                                                                                                                                cDNA; 5567
                                                                                                                                                                                                                                                                                                                                                                                                                                6.3%;
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; Pred. No. 8.7,
0; Mismatches
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                                                                                                   Math4B)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  367 T; 0 other;
                                                                                                  CDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                  7e-35;
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                                                                                                   SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1861;
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                                                                                                   NO:4.
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                                                                                                                                                                                       RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Human; splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease related to loss of a functional atonal-associated nucleic acid on protein. They may particularly be used to treat an animal with a deficiency in cerebellar granule neurons or their precursors, and may also be used in promoting mechanoreceptive cell growth and generating hair cells. The present sequence represents an atonal-associated nucleic acid sequence referred to in the invention.

Note: The present sequence is not shown in the specification, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression of an atonal-associated nucleic acid sequence in an animal, and a transgenic animal in which an allele of a native atonal-associated gene is replaced by a heterologous nucleic acid sequence, thus inactivating the atonal-associated allele. The nucleic acids or proteins may be used in a method of treating an animal for hearing impairment, joint disease, balance disorders, abnormal cell proliferation, or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid sequence, or any of its homologues or orthologues as therapeutic agents for the treatment of deafness, partial hearing vestibular effects due to damage or loss of inner hair cells, osteoarthritis and abnormal cell proliferation. The invention also encompasses methods of screening for compounds which affect the
                                                   Rat spliced
                                                                                                                                                     ABN31392 standard; DNA; 65
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to the use of atonal-associated nucleic acid or amino acid sequence, or any of its homologues or orthologues as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page -; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          any of its homologs or orthologs, for the treatment osteoarthritis and abnormal cell proliferation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Therapeutic use of atomal associated nucleic acids or amino acids, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zoghbi HY, Bellen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1999; 99US-0137060.
19-JAN-2000; 2000US-0176993.
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                                                                                    15-JUL-2002
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                                                                                                                                                                                                                                                                                                             5226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   obtained from GenBank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-032190/04.
                                                                                                                                                                                                                                                                          822
                                                                                                                                                                                                                                                                                                                                                                              92;
mouse; rat; splice transcript; detection; RNA transcript;
variant; transcriptome; oligonucleotide library; ss.
                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                            ATCGAGACCCTGCGCTTCGCCCACAACTACAT 5317
                                                                                                                                                                                                                                                               ATCGAGACCCTGCGCTTCGCCCACAACTACAT
                                                                                                                                                                                                                                                                                                             GCGCTGGATGCGCTGCGCGCTGCCCCACCTTCCCGGATGACGCCAAACTTACAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 5567
                                                 transcript detection oligonucleotide SEQ ID NO:4140.
                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                               BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                               1271 A; 1549 C;
                                                                                                                                                                                                                                                                                                                                                                                            6.3%;
100.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               1564 G; 1183 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hassan
                                                                                                                                                                                                                                                                                                                                                                                              DB 22; I
8.3e-35;
                                                                                                                                                                                                                                                                          853
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                                                                                                                                                                                                                                                                                                                                                                                                            Length 5567;
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                                                                                                                                                                                                                                                                                                                                                                              0;
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15-JUL-2002

(first entry)

Human; mouse; rat; splice transcript; detection; RNA transcript; splice variant; transcriptome; oligonucleotide library; ss.

Mouse spliced transcript detection oligonucleotide SEQ ID NO:30269

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ATTGCAGGCTGATCTCCTCTTAACCCTCCTCAGTGT

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ABN57521 RESULT 10

ABN57521 standard; DNA; 65 BP

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                                                                                                                                 Query Match
Best Local S
Matches 36
                                                                                                                                                                                                                                            quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue- and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonuclectide sequences from rats, humans and mice, which are used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                             several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or
                                                                                                                                 Sequence 65 BP; 11 A; 20 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUL-2000;
02-MAY-2001;
                                                                                                                                                                       at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                          the exemplification of the present invention.
N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes oligonucleotide libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID 4140; 47pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shoshan A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JUL-2001; 2001WO-IB01903.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (COMP-) COMPUGEN INC
                                                                      Local Similarity
1281 ATTGCAGGCTGATCTCCTCTTAACCCTCCTCAGTGT 1316
                                                      36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wasserman A,
                                                        Conservative
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2001US-287724P.
                                                                      2.5%;
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                                                      0;
                                                                                                                                 14 G; 20 T; 0 other;
                                                                      Score 36; DB 24;
Pred. No. 3.2e-07;
                                                        Mismatches
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                                                                                           Length 65,
                                                        Indels
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                                                        Gaps
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RESULT 11
AAD46890
     SEXEXEXEX
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                                                                                                                                                                                                                                                                                                                                                                               the genome, which encodes one or more messenger RNA splice variants.

CC The oligonuclectide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in CC detecting RNA transcripts and splice variants of human or animal CC transcriptomes. The libraries may also be used as specialised mini CC libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the CC particular biological or pathology-specific genes such as those genes CC only expressed in specific tissue under a specific pathological condition, to detect developmental specific genes such as those genes CC condition, to detect developmental specific genes; and to detect RNA CC transcripts and splice variants of a transcriptome of a patient suffering CC oligonucleotide sequences from rats, humans and mice, which are used in the sequence data for this patent did not form part of the printed care transcriptome of the present invention.
                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger NAS transcribed from multipl transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to several oligonucleotides, each capable of hybridising selectively to set of messenger RNAs transcribed from a given transcription unit of the second several oligonucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription a genome, useful for detecting tissue-, pathology-, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
Human; transcription factor; neuroendocrine basic helix-loop-helix; type 2 diabetes mellitus; autoimmune destruction; type 1 diabetes;
                                                   Human neurogenin 2 (Ngn2) gene #1.
                                                                                                                                                      AAD46890 standard; DNA; 6123 BP
                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUL-2000;
02-MAY-2001;
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                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                           547
                                                                                                                                                                                                                                                                                                            35;
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                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                         2.4%;
llarity 100.0%;
Conservative (
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2001US-287724P.
                                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                               P
                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                               25 C;
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                                                                                                                                                                                                                                                                                                            <u>.</u>.
                                                                                                                                                                                                                                                                                                                                                                              11 G; 13 T; 0 other;
                                                                                                                                                                                                                                                                                                                          Score 3
                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                            35;
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                                                                                                                                                                                                                                                                                                                          DB 24; I
9.8e-07;
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                                                                                                                                                                                                                                                                                                                                              65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        multiple
                                                                                                                                                                                                                                                                                                            Gaps
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RESULT 12
AAC61089
ID AAC61
XX AC61
AC AAC61
XX O5-FE
XX Neuro
XX Neuro
XX Neuro
XX islet
XX islet
XX Homo
XX 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method for producing a mammalian islet cell. The method comprising introducing into a mammalian cell a nucleic acid molecule encoding an islet transcription factor for expression of the islet transcription factor in the cell and for production of islet cell phenotype in the cell. The islet transcription factor is a neuroendocrine basic helix-loop-helix (bHLH) transcription factor. The method is useful for treating type 2 diabetes mellitus and for replacing beta cells lost to autoimmune destruction in individuals with type 1 diabetes. The method is useful in cell therapy. The present sequence is human neurogenin 2 (Mrm.) Care
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Producing a mammalian islet cell for treating diabetes mellitus comprises introducing into a mammalian cell a nucleic acid molecule encoding neuroendocrine basic helix-loop-helix transcription factor
                                                                                                                                                                                               Neurogenin
islet cell
                                                                                                                                                                                                                                                                                 Human neurogenin 3 (Ngn3) genomic DNA sequence
                                                                                                                                                                                                                                                                                                                                        05-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC61089 standard; DNA; 5340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6123 BP; 1484 A; 1536 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 95-97; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAR-2002; 2002WO-US11166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200274045-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              islet cell; cell therapy; neurogenin 2; Ngn2; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Ngn2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                        sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002-759853/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGATCGAGACCCTGCGCTTCGCCCACAACTACAT 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGATCGAGACCCTGCGCTTCGCCCACAACTACAT 853
                                                                                                                                                                                             3; Ngn3; chromosome 10q22.1-22.2; cellular differentiation; precursor identification; diabetes mellitus; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.4%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001US-0817360
                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /partial
                                                    Location/Qualifiers
  /product= "Ngn3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "Human Ngn2 p
/note= "No start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Human Ngn2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G; 1596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 24;
8.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 6123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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RESULT 13
AAD46871
ID AAD46
XX AAD46
XX AAD46
XX Humar
XX Humar
XX Humar
XX Humar
XX Homo
CX EW Sene;
XW Cypee
KW islet
XX Sene;
XX Homo
XX Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                망
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The human neurogenin 3 Ngn3 DNA sequence AAC61089 encodes the Ngn3 protein AAV85617. The Ngn3 gene is located at chromosome position 10q22.1-22.2. The invention relates to the human Ngn3 nucleotide and protein sequences, and includes an antibody recognising the Ngn3 protein. Also included in the invention is a method for identifying an islet cell precursor, the method involves analysing a cell for the expression of the Ngn3 gene product, where detection of the product is indicative of an islet cell precursor. The Ngn3 DNA sequence is useful as a diagnostic reagent for detecting (in a subject) a predisposition to a defect in pancreatic islet cell function or formation associated with a defect in Ngn3 activity. The Ngn3 protein is useful for identifying beta-cell precursor cells expressing Ngn3, and to alter cellular differentiation in culture in vivo to produce new beta-cells to treat patients with diabetes
                                   WO200274045-A2
                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                            Human; transcription factor; neuroendocrine basic helix-loop-helix; bHLH; type 2 diabetes mellitus; autoimmune destruction; type 1 diabetes; islet cell; cell therapy; neurogenin 3; Ngn3; chromosome 10q22.1-22.2; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human neurogenin 3 (Ngn3) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD46871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD46871 standard; DNA; 5340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 6; Page 46-48; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   them, useful for diagnosis, prevention and treatment of diabetes mellitus and to identify individuals at risk of diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human neurogenin 3 polypeptides and polynucleotides encoding them, useful for diagnosis, prevention and treatment of diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          German MS, Lin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-MAR-2000; 2000WO-US08436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200059936-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000-664989/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
32; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGAGCGAGTTGGCACTGAGCAAGCAGCGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGAGCGAGTTGGCACTGAGCAAGCAGCGACG 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0128180
                                                                                                                                                      Location/Qualifiers 3022..3666
                                                                                         /*tag= a
/product= "Human Ngn3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "Neurogenin 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1215 A; 1500 C; 1514 G; 1111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.2%; Score 32; DB
100.0%; Pred. No. 2.4
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Β₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.4e-05;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 5340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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RESULT 14
AAS33797
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method for producing a mammalian islet cell. The method comprising introducing into a mammalian cell a nucleic acid molecule encoding an islet transcription factor for expression of the islet transcription factor in the cell and for production of islet cell phenotype in the cell. The islet transcription factor is a neuroendocrine basic helix-loop-helix (bHLH) transcription factor. The method is useful
                                                                                                                                                                                                                         cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Producing a mammalian islet cell for treating diabetes mellitus comprises introducing into a mammalian cell a nucleic acid molecule encoding neuroendocrine basic helix-loop-helix transcription factor
          24-FEB-2000;
02-MAR-2000;
                                        31-JAN-2000;
04-FEB-2000;
                                                                                                                                                                                                                                                                                    cardiovascular; autoimmune disease; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                              Human cDNA encoding a novel foetal antigen,
                                                                                                                                                                                                                                                                                                                                                                           17-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for treating type 2 diabetes mellitus and for replacing beta cells lost to autoimmune destruction in individuals with type 1 diabetes. The method is useful in cell therapy. The present sequence is buman neurogenin 3 (Ngn3) gene. Ngn3 gene is located on chromosome 10q22.1-22.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-MAR-2002; 2002WO-US11166
                                                                                       17-JAN-2001;
                                                                                                                   02-AUG-2001
                                                                                                                                                 WO200155312-A2
                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                      hyperproliferative disorder; breast neoplasm; cancer;
                                                                                                                                                                                                                                                                                                                Human; foetal tissue antigen; ss; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS33797 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-MAR-2001; 2001US-0817360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-SEP-2002
                                                                                                                                                                                                                                                                                                  immunomodulator; cardiovascular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002-759853/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            672
                                                                                                                                                                                                         healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.2%;
Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Page 87-88; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE29277.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGAGCGAGTTGGCACTGAGCAAGCAGCGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGAGCGAGTTGGCACTGAGCAAGCAGCGACG 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5340 BP; 1215 A; 1500 C; 1514 G; 1111 T; 0 other;
         2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-0186350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                       2001WO-US01321.
                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                           epithelial cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                  cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3266
                                                                                                                                                                                                                                                                                                                                              SEQ
                                                                                                                                                                                                            food additive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 5340;
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                                                                                                                                                                                                                                                                                                                  neuroprotective;
                                                                                                                                                                                                                                                                                                                                               321.
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13-OCT-2000
20-OCT-2000
20-OCT-2000
20-OCT-2000
20-OCT-2000
20-OCT-2000
20-OCT-2000
20-OCT-2000
08-NOV-2000
01-NOV-2000
01-NOV-2000
01-NOV-2000
01-NOV-2000
01-DEC-2000
01-DEC-2000
08-DEC-2000
         Claim
                                     New polynucleotides and polypeptides for diagnosing, treating, preventing or prognosing e.g. diseases or disorders of the nervous, musculoskeletal, excretory, gastrointestinal, reproductive, and
                            respiratory
                                                                             WPI; 2001-488782/53.
P-PSDB; AAU20977.
                                                                                                            ÇĄ,
                                                                                                                                 HUMAN
                                                                                                            Barash
                             systems
                                                                                                                                                   2000US-0241785

2000US-0241786

2000US-0241808

2000US-02441809

2000US-0244617

2000US-0246476

2000US-0246476

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2000US-0246477

2000US-0246523

2000US-0246524

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2000US-0249211

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2000US-0249216

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2000US-0249216

2000US-0251030

2000US-02511030

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2000US-0251198

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2000US-0251198
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2000US-0240960.
2000US-0241221.
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                                                                                                            Ruben
       642pp;
                                                                                                                                 INC
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SEQ

ID No

321;

English.

17. MAR-2000
19. MAY-2000
19. MAY-2000
20. JUIN-2000
20. JUIN-2000
20. JUIN-2000
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21. JUIN-2000
21. JUIN-2000
22. AUG-2000
23. JUIN-2000
24. AUG-2000
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25. SEP-2000
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27. SEP-2000
29. SEP-2000
20. SEP-20

2000US-0199076
2000US-0199076
2000US-0205515
2000US-0205515
2000US-0205515
2000US-0216647
2000US-0216647
2000US-0216647
2000US-0216647
2000US-0217496
2000US-0217496
2000US-0217496
2000US-0225513
2000US-02255214
2000US-02252521
2000US-02252521
2000US-0225757
2000US-0225775
2000US-0225776
2000US-0225778
2000US-0225778
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2000US-0225778
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2000US-0225779
2000US-0237777

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RESULT 15
ABT03700/c
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel nucleic acids encoding novel human foetal antigens. The nucleic acids and proteins are used to prevent, treat (e.g by gene therapy) or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. The antibodies to the antigens can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunoasobent assays (ELISA). Disorders which are diagnosed or treated induncations of the condition of the condition are diagnosed or treated include authorities.
                                                                                                                                               Determining the presence of neoplastic molecular markers, by identifying the presence of markers in host test sample using neoplastic molecular marker specific reagents and analyzing the
                                                                                                                                                                                                                                         WPI; 2002-537346/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200240716-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cancer; neoplastic disease; tumour specific marker; cytostatic; transcription factor; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Neurogenin-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABT03700 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. Numerous examples of diseases and disorders treated by the nucleic acids and proteins are given in the specification. The present sequence
                                                                                Example 1; Page 17; 41pp; English
                                                                                                                                                                                                                                                                                       Palm
                                                                                                                                                                                                                                                                                                                                                                             16-NOV-2000; 2000US-249508P
                                                                                                                                                                                                                                                                                                                                                                                                                      13-NOV-2001; 2001WO-US43461
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                                                                                                                            reagents
                                                                                                                                                                                                                                                                                                                                 CEMINES LLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.0008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NO: 221.
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                                                                                                                                                                        array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                        of.
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The present invention relates to a method for determining the presence one operatic molecular markers in a host, involving the use of neoplastic molecular marker specific reagents to detect such markers and analysing

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AACCTTAACTCCGCGCTGGATGCGC

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            Query Match
Best Local :
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 Matches
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Best Local
                                                                                         PCR primers AAV42515-16 are used to isolate part of the DNA encoding a basic helix-loop-helix (BHLH) type protein, designated RELAX (Rat Embryonic Longitudinal Axis) protein. The PCR product is termed CIG235. The protein is used to control and participate in gene expression, by acting as transcriptional activator, strictly dependent on the presence of an intact E box (CANNTG), particularly for targeting expression of proteins to the central nervous system (CNS). The nucleic acid sequence can be used to treat nervous system disorders,
                                                                                                                                                                                                                                             Basic helix-loop-helix polypeptide and related nucleic acid - v transcriptional activity, for targeting expression of genes to central nervous system and treatment of nervous disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Basic helix-loop-helix; BHLH; RELAX; Rat Embryonic Longitudinal control; gene expression; transcriptional activator; targeting; protein expression; central nervous system; CNS; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the array of reagents, allowing the identification of the neoplastic disease present. This can be used to determine the best treatment for cancers, in particular neural cell, lung and prostate tumours. The present sequence is a PCR primer useful for detecting the coding
                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV42515 standard; DNA; 25 BP
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                                                                                                                                                                                                                      Example 2;
                                                                                                                                                                                                                                                                                                      WPI; 1998-362775/31.
                                                                                                                                                                                                                                                                                                                                                                                                                19-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nervous system disorder; CIG235; PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR primer used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV42515;
                                                                                                                                                                                                                                                                                                                                                          (RHON ) RHONE-POULENC RORER SA
                                                                                                                                                                                                                                                                                                                                                                                     19-DEC-1996;
                                                                                 antisense
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26; Conserv
 25;
               Similarity
                                                      25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 BP; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of markers of the invention.
                                                                                                                                                                                                                      Page 12; 28pp; French.
                                                                                                                                                                                                                                                                                                                               Ravassard P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.8%;
ilarity 100.0%;
Conservative
Conservative 0;
                                                      BP; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                               sequences can be used to control
                                                                                                                                                                                                                                                                                                                                                                                     96FR-0015651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isolate part of the RELAX protein coding region.
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                                                      9 C; 6 G; 5 T; 0 other;
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G;
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               Score 25;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 26;
Pred. No.
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  Mismatches
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0.027;
                           DB 19;
               0.083;
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  <u>.</u>
                           Length 25;
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Indels
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AACCTTAACTCCGCGCTGGATGCGC 25

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RESULT 18
AAZ51977
ID AAZ51
XX
AC AAZ51
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AC AAZ51
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DT 04-JU
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Best Local
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27-SEP-1996;
12-NOV-1996;
19-DEC-1996;
                                                                                                                                                                                                                                                            The
         Murine neurogenin-1 (NGN1) nucleic
                              04-JUL-2000
                                                                    AAZ51977 standard; DNA; 738 BP
                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                   the present invention. The neurogenin nucleic acids can be expressed a host cell, transformed using an expression vector, to produce recombinant proteins. The proteins and the antibodies raised against the proteins are useful in the study of neurogenesis.
                                                                                                                                                                                                                                                                               Claim 5; Fig 4; 106pp;
                                                                                                                                                                                                                                                                                                 Mouse neurogenins, useful in neurogenesis - and acids and proteins derived from rat and Xenopus
                                                                                                                                                                                                                                                                                                                                           WPI; 1998-230702/20.
                                                                                                                                                                                                                                                                                                                                                              Anderson DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV27046;
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                                                                                                                                                                                                                                                                                                                                                                                (CALY ) CALIFORNIA INST OF TECHNOLOGY.
                                                                                                                                                                    Local
                                                                                                                                                                                                                                                          mouse neurogenin 1 is one of several neurogenin proteins discussed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse;
                                                                                                                     304
                                                                                                                                        732
                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                 AAW54944.
                                                                                                                    GAGCGCAACCGCATGCACAACCT 326
                                                                                                                                        GAGCGCAACCGCATGCACAACCT 754
                                                                                                                                                                                                  738 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neurogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurogenin;
                                                                                                                                                          Conservative
                             (first entry)
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96US-0030864.
96US-0772009.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/product= "Mouse neurogenin
                                                                                                                                                                                                 121 A; 283 C; 205 G; 129 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                              Sommer L;
                                                                                                                                                                               1.6%;
                                                                                                                                                                                                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression vector; recombinant protein;
                                                                                                                                                       0;
                                                                                                                                                                    Score 23; Pred. No.
                                                                                                                                                           Mismatches
         acid sequence
                                                                                                                                                                    DB 19;
                                                                                                                                                          ٥,
                                                                                                                                                                              Length 738;
                                                                                                                                                                                                                                                                                                             recombinant nucleic
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RESULT 19 AAF27264

AAF27264 standard; cDNA; 790

ВP

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24-APR-2001

(first entry)

Chicken atonal homologue ngn2/ath4a cDNA,

SEQ ID

NO:20

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                                                                                                                                        Matches
                                                                                                    Query Match
                                                                                     Best Local
                                                                                                                                                                                                                      specific marker. Transformed host cells are used as sources of neuronal and other growth factors; in culture for screening compounds that modulate neural differentiation or as sources of recombinantly produced neurogenins and Phox2a proteins for use in transplantation. The cells also have a variety of in vivo uses, e.g. for transplantation at sites o neuronal dysfunction e.g. pattents with hearing or vision loss due to optical or auditory nerve damage, brain or spinal cord injuries, and neurodegenerative disorders e.g. Alzheimer's disease. The present sequence encodes murine neurogenin-1 (NGN-1), a transcription factor.

NNCs differentiate into neurons through the recombinant expression of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neurogenin-1; NGN-1; non-neuronal cell; NNC; neurogenesis; Phox2a protein; neuronal subtype-specific marker; growth factor; perval differentiation; transplantation; neuronal dysfunction; optical nerve damage; auditory nerve damage, neurodegenerative disorder; neuroprotective; nootropic; anticonvulsant; antiParkinsonian; vulnerary;
                                                                                                                                                                       transcription factor that induces a core program of neurogenesis. Forced expression of murine NGN1 can elicit expression of at least some neuronal phenotypic markers even in NNCs. This can be used in autografting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inducing non-neuronal cells to differentiate into neurons and for non-neuronal cells to express a neuronal subtype-specific marker, comprising contacting the non-neuronal cells with a vector containing neurogenin nucleic acid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                     The patent discloses a method for inducing non-neuronal cells (NNC) differentiate into neurons and for NNCs to express a neuronal subty
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 1C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cerebroprotective; immunesuppressant; antiinfectious; ss.
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 304
                                732 GAGCGCAACCGCATGCACAACCT 754
                                                                   l Similarity
23; Conserv
GAGCGCAACCGCATGCACAACCT 326
                                                                                                                                        738 BP;
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                                                                                                                                      121 A; 283 C; 205 G; 129 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= "Murine neurogenin-1 protein"
                                                            1.6%; bu
/ 100.0%; Prr
                                                                                   Score 23;
Pred. No.
                                                                     Mismatches
                                                                                                      DB 21;
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                                                                                                                                                               RESULT 20
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                                                                                                                                                                                                                                                                                                                                                                                        and a transgenic animal in which an allele of a native atonal associated gene is replaced by a heterologous nucleic acid sequence, thus inactivating the atonal associated allele. The nucleic acids or proteins may be used in a method of treating an animal for hearing impairment, joint disease, balance disorders, abnormal cell proliferation, or other disease related to loss of a functional atonal associated nucleic acid or protein. They may particularly be used to treat an animal with a deficiency in cerebellar granule neurons or their precursors, and may also be used in promoting mechanoreceptive cell growth and generating hair cells. The present sequence represents an atonal-associated nucleic acid sequence referred to in the invention.

Note: The present sequence is not shown in the specification, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid sequence, or any of its homologues or orthologues as therapeutic agents for the treatment of deafiness, partial hearing loss, vestibular effects due to damage or loss of inner hair cells, osteoarthritis and abnormal cell proliferation. The invention also encompasses methods of screening for compounds which affect the expression of an atomal-associated nucleic acid sequence in an animal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Therapeutic use of atonal-associated nucleic acids any of its homologs or orthologs, for the treatment osteoarthritis and abnormal cell proliferation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Atonal; homologue; orthologue; atonal-associated protein; deafness; hearing impairment; vestibular effect; balance disorder; osteoarthritis; cellular proliferation; cerebellar granule neuron; gene therapy; mechanoreceptive cell growth; auditory; osteopathic; cytostatic;
           DNA encoding murine neuroD3
                                              25-MAR-2003
21-OCT-1998
                                                                                                                            AAV42938 standard;
                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page -; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zoghbi
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19-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                               obtained from GenBank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to the use of atonal-associated nucleic acid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-032190/04.
                                                                                                                                                                                                              374
                                                                                                                                                                                                                                                 732
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                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                 GAGCGCAACCGCATGCACAACCT 754
                                                                                                                                                                                                              GAGCGCAACCGCATGCACAACCT 396
                                                                                                                                                                                                                                                                                                                                               790 BP; 91 A; 351 C;
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2000US-0176993.
                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                              DNA;
                                            entry)
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             protein,
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                                                                                                                                                                                                                                                                                               Score 23;
Pred. No.
                                                                                                                                                                                                                                                                                                                                               283 G; 65
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               18
           a bHLH protein.
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                                                                                                                                                                                                                                                                                                              Length 790;
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E e.g. deafness,
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RESULT 21
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Matches
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02-NOV-1995;
30-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neuroectodermal tumours. The method comprises measuring, in a tumour sample, expression of at least one basic bHLH gene and identifying tumour subclass by matching expression to predetermined expression profiles for known subclasses. For classifying the tumour as a medulloblastoma, the bHLH gene detected is neuroDl and neuroD3. The method is used to classify neuroectodermal tumours, and to iden medullablastoma and for prognosis of this as aggressive. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes a protein which is a member of the basic helix-loop-helix (bHJH) protein family, and is designated neuroD3. The bHJH genes are a family of genes ared with vertebrate neuronal, endocrinal and gastrointestinal development. The observed pattern of neuroD expression distinguishes subclasses of neuroectodermal tumours. The specification describes a method for the classification of human the specification describes a method for the classification of human.
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Mouse; gene; ds; neuroD3; neuroD; basic-helix-loop-helix; differentiation; neurone; endocrine; gastrointestine; deve transgenic; embryo; birth defect; spontaneous abortion; st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Classifying neuroectodermal tumours from expression pattern of basic-helix-loop-helix genes - especially foor identifying medulla:blastoma and assessing its aggressiveness, specifically associated with expression of BHLH genes neuroD 1-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Olson JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-AUG-1997;
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                                                                                                                  Mouse bHLH
                                                                                                                                                                          23-JAN-2003
                                                                                                                                                                                                                                                                                          ABS56396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB;
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23; Conserv
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                                                                                                                                                                                                                                                                                          standard; DNA; 1332
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                                                                                                                  family neuroD3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.6%; Score 23; llarity 100.0%; Pred. No. Conservative 0; Mismatc
                                                                                                                                                                       (first entry)
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95US-0552142.
96WO-US17532.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268 A; 452 C;
                                                                                                                  genomic DNA.
                                                                                                                                                                                                                                                                                          ВP
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0.67;
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                                development;
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08-MAY-1995;
02-NOV-1995;
30-OCT-1996;
                                                                                                                                                                                                                                                                                                                                             those that are active in development and cancer. The resultant cell lines find use as sources of novel neural growth factors, in assays for identifying novel neuranal growth factors which can be used for screening anti-cancer drugs capable of driving terminal differentiation in neural tumours, for producing antibodies useful in diagnostic assays and for screening for compounds capable of modulating the activity of neural for transformed host cells, nucleic acids and polypeptides are also useful for treating sites of traumatic neural injury where motor or sensory neural activity has been lost, e.g. hearing or vision loss and brain or spinal cord damage. The host cells find use in the treatment of malabsorption syndromes or gastrointestinal dysmotility syndromes (Hirsh prung's Disease). The cell lines also find use in screening for candidate correcting the cellular defect caused by a defective neuroD or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          implicated in the regulation of differentiation. NeuroD proteins are particularly involved in neuronal, endocrine and gastrointestinal development. The nucleic acid is useful for constructing recombinant cell lines, transgenic embryos and animals and for quantifying the level of expression of neuroD in a cell. Birth defects and spontaneous abortions may result from expression of an abnormal neuroD protein. The polynucleotide sequences permit the establishment of primary cultures of proliferating embryonic neuronal stem cells under conditions minicking the proliferating embryonic neuronal stem cells under conditions minicking the setablishment of primary cultures of proliferating embryonic neuronal stem cells under conditions minicking the proliferating embryonic neuronal stem cells under conditions minicking the particle sequences primary cultures of proliferating embryonic neuronal stem cells under conditions minicking the setablishment of primary cultures of proliferating embryonic neuronal stem cells under conditions minicking the setablishment of primary cultures of proliferating embryonic neuronal stem cells under conditions minicking the level of the setablishment of primary cultures of proliferating embryonic neuronal stem cells under conditions minicking the level of the setablishment of primary cultures of proliferating embryonic neuronal stem cells under conditions minicking the setablishment of primary cultures of proliferating embryonic neuronal stem cells under conditions minicking the setablishment of primary cultures of prima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     functionally active human neuroD3 polypeptide. NeuroD proteins represent a new family within the basic-helix-loop-helix (bHLH) family which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New neurogenic differentiation gene, useful in gene therapy to correct traumatic neural injury that has resulted in loss of motor or sensory neural function and for constructing recombinant cell lines -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer; neural growth factor; tumour; diagnostic; motor; sensory; traumatic neural injury; hearing; vision; brain; spinal cord; malabsorption syndrome; gastrointestinal dysmotility syndrome; Hirsh Prung's disease; therapeutic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 11; Column 75-78; 43pp; English.
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                                                                                                                                                                                                               Sequence 1332 BP;
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l Similarity
23; Conserv
                                                                                                                                                                                                                                                                                                                  18
                                                                                                                                                                                                                                                                                                            the mouse neuroD3 genomic DNA.
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95US-0552142.
96WO-US17532.
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                                                                                                                                                                                                    268 A; 452 C; 352 G; 260 T; 0 other;
                                           1.6%; Score 23;
100.0%; Pred. No.
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                                           DB 25;
0.67;
                                                                                             Length 1332;
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RESULT 22
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                                                 Matches
                                                                       Query Match
                                                                                                                       basic helix loop helix (bHLH) transcriptional activators involved in neuronal, endocrine and gastrointestinal development. They were discovered by expression cloning and screening assays designed to identify possible bHLH proteins capable of interacting with the protein product of the Drosophila daugherless gene. Novel neuroD2 and neuroD3 genes, related to neuroD1, have been identified. NeuroD nucleic acids can be used to produce NeuroD polypeptides, construction of test cell lines, as probes, in gene therapy, and to produce transgenic animals as models of disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT74894 standard; cDNA; 1333
                                                                                                 Sequence 1333
                                                                                                                                                                                                                                                                                                                                  Nucleic acid encoding neus
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                                                                                                                                                                                                                                       Neurogenic differentiation (NeuroD) genes (AAT74887-94) and pro
(AAW22436-43) from human, mouse and frog have been identified,
isolated and sequence. NeuroD polypeptides are tissue-specific
                                                                                                                                                                                                                                                                                           Claim 1; Page 72-74; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAW22443.
                                                                                                                                                                                                                                                                                                                                                                                                               Hollenberg SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neurogenic differentiation protein; NeuroD; neuroD3 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse neurogenic
                                                                                                                                                                                                                                                                                                                       development
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-272117/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9716548-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transcriptional activator; neuron; pancreas; gastrointestine; knock-out mouse; transgenic animal; cancer; diabetes; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                        (WEIN/) WEINTRAUB N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUTC-) HUTCHINSON CANCER RES CENT FRED
                                                             Local
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                                                             Similarity
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GAGCGCAACCGCATGCACAACCT 426
                       GAGCGCAACCGCATGCACAACCT 754
                                               Conservative
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                                                                                                  BP;
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                                                                                                                                                                                                                                                                                                                                                                                                               Lee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         differentiation protein (NeuroD3)
                                                                                                  268 A; 452 C; 353 G;
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                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                               neurogenic
                                                                         1.6%;
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                                                                                                                                                                                                                                                                                                                                   neuronal,
                                               0;
                                                           Score 23;
Pred. No.
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                                                 Mismatches
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al, endocrine and gastrointestinal
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                                                                                                 260 T; 0 other;
                                                                         DB 18;
                                                             0.67;
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                                                                         Length 1333;
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RESULT 23
AAVZ7049
ID AAVZ77049
ID AAVZ77
XX AVZ7
XX AVZ7
XX MOUSE
XX MOUSE
XX MUS E
YT CDS
FT CDS
F
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AAZ51980
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12-NOV-1996;
19-DEC-1996;
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Neurogenin-2; NGN-2; non-neuronal cell; NNC; neurogenesis; Phox2a protein; neuronal subtype-specific marker; growth factoneural differentiation; transplantation; neuronal dysfunction;
                                                                     Murine neurogenin-2
                                                                                                          04-JUL-2000
                                                                                                                                                                               AAZ51980 standard; DNA; 1385
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1385 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 in the present invention. The neurogenin nucleic acids can be in a host cell, transformed using an expression vector, to prove the proteins. The proteins and the antibodies raised the proteins are useful in the study of neurogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Fig 7; 106pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anderson DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ds; Mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse neurogenin 2 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV27049 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CALY ) CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse neurogenin 2 is one of several neurogenin proteins discussed the present invention. The neurogenin nucleic acids can be expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1998-230702/20
                                                                                                                                                                                                                                                                       742
                                                                                                                                                                                                                                                                                                           732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neurogenins,
and proteins
                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                       GAGCGCAACCGCATGCACAACCT 764
                                                                                                                                                                                                                                                                                                       GAGCGCAACCGCATGCACAACCT 754
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96US-0722570.
96US-0030864.
96US-0772009.
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382..1173
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                                                                                                                                                                                                                                                                                                                                                                                                                  242 A; 467 C; 432 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful in neurogenesis - and recombinant nucleic derived from rat and Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INST OF TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry
                                                                     (NGN-2) nucleic acid sequence.
                                                                                                          entry)
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                                                                                                                                                                                                                                                                                                                                                                                1.6%;
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optical nerve damage; auditory nerve damage, neurodegenerative disorder; neuroprotective; nootropic; anticonvulsant; antiParkinsonian; vulnerary; cerebroprotective; immunesuppressant; antiinfectious; ds.
Mus sp.
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Location/Qualifiers 382..1173 *tag=

/product= "Murine neurogenin-2 protein

WO200009676-A2

24-FEB-2000

13-AUG-1999; 99WO-US18525

14-AUG-1998; 98US-0096630

(CALY) CALIFORNIA INST OF TECHNOLOGY.

Anderson DJ, ç

2000-256250/22.

Inducing non-neuronal cells to differentiate into neurons and for non-neuronal cells to express a neuronal subtype-specific marker, comprising contacting the non-neuronal cells with a vector contain neurogenin nucleic acid containing

Claim 1; Fig 1I; 76pp; English.

neuronal dysfunction e.g. patients with hearing or vision loss due to optical or auditory nerve damage, brain or spinal cord injuries, and neurodegenerative disorders e.g. Alzheimer's disease. The present sequence encodes murine neurogenin-2 (NGN-2), a transcription factor. NNCs differentiate into neurons through the recombinant expression of a transcription factor that induces a core program of neurogenesis. Forced expression of murine NGN2 can elicit expression of at least some neuronal The patent discloses a method for inducing non-neuronal cells (NNC) to differentiate into neurons and for NNCs to express a neuronal subtype specific marker. Transformed host cells are used as sources of neuronal and other growth factors; in culture for screening compounds that modulate neural differentiation or as sources of recombinantly produced neurogenins and Phox2a proteins for use in transplantation. The cells also have a variety of in vivo uses, e.g. for transplantation at sites of phenotypic markers even in NNCs.

Sequence 1385 BP; 242 A; 467 C; 432 G; 244 T; 0 other;

Best Loc Matches Query Match Local l Similarity 23; Conser 1.6%; nilarity 100.0%; Conservative 0 0 Score 23; ; Pred. No. Mismatches DB 0.67; 21; 0, Length 1385; Indels 0 Gaps

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RESULT 25

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742 732

GAGCGCAACCGCATGCACAACCT

754

GAGCGCAACCGCATGCACAACCT 764

AAF27269 AAF27269 standard; cDNA; ВP

24-APR-2001 (first entry)

Mouse neurogenin 2 (ngn2) cDNA, SEQ ID NO:30.

TXXXXXXXXXXXX Atonal; homologue; orthologue; atonal-associated protein; deafness; hearing impairment; vestibular effect; balance disorder; osteoarthr cellular proliferation; cerebellar granule neuron; gene therapy; osteoarthritis;

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ARESULT 26
AAF27255
ID AAF277
XX AAF27
XX AAF27
XX AAF27
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XX AOU86
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KW Heart
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                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to the use of atomal-associated nucleic acid or CC amino acid sequence, or any of its homologues or orthologues as CC therapeutic agents for the treatment of deafness, partial hearing loss, CC vestibular effects due to damage or loss of inner hair cells, CC osteoarchritis and abnormal cell proliferation. The invention also cencompasses methods of screening for compounds which affect the CC expression of an atomal-associated nucleic acid sequence in an animal, and a transgenic animal in which an allele of a native atomal-associated CC gene is replaced by a heterologous nucleic acid sequence, thus consider the atomal-associated allele. The nucleic acids or proteins may be used in a method of treating an animal for hearing impairment, CC joint disease, balance disorders, abnormal cell proliferation, or other CC disease related to loss of a functional atomal-associated nucleic acid or protein. They may particularly be used to treat an animal with a considering in cereballar granula neurons or their precursors, and may call sequence represents an atomal-associated nucleic acid or the invention.

CC deficiency in cereballar granula neurons or the received in the invention.
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                               Matches
Atonal; homologue; orthologue; atonal-associated protein; deafness; hearing impairment; vestibular effect; balance disorder; osteoarthr; cellular proliferation; cerebellar granule neuron; gene therapy; mechanoreceptive cell growth; auditory; osteopathic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Therapeutic use of atonal-associated nucleic acids or amino acids, or any of its homologs or orthologs, for the treatment of e.g. deafness, osteoarthritis and abnormal cell proliferation -
                                                                                           Mouse atonal
                                                                                                                            24-APR-2001
                                                                                                                                                                                                 AAF27255 standard; cDNA; 1412
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1385 BP;
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19-JAN-2000; 2000US-0176993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-032190/04.
                                                                                                                                                                                                                                                                                                                          732 GAGCGCAACCGCATGCACAACCT 754
                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                       homologue 4 (ATOH4, Math4A) cDNA,
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                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence is not shown GenBank.
                                                                                                                                                                                                                                                                                                                                                                                                                                 242 A; 467 C; 432 G;
                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                              Mismatches
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0.67;
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                                                                                         ID NO
                                 osteoarthritis;
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ARESULT 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to the use of atonal-associated nucleic acid or CC amino acid sequence, or any of its homologues or orthologues as CC therapeutic agents for the treatment of deafness, partial hearing loss, CC vestibular effects due to damage or loss of inner hair cells, CC osteoarthritis and abnormal cell proliferation. The invention also CC encompasses methods of screening for compounds which affect the cC expression of an atonal-associated nucleic acid sequence in an animal, CC and a transgenic animal in which an allele of a native atonal-associated CC gene is replaced by a heterologous nucleic acid sequence, thus CC inactivating the atonal-associated allele. The nucleic acids or proteins CC inscription and method of treating an animal for hearing impairment, CC joint disease, balance disorders, abnormal cell proliferation, or other CC disease related to loss of a functional atonal-associated nucleic acid or grotein. They may particularly be used to treat an animal with a CC deficiency in cerebellar granule neurons or their precursors, and may CC also be used in promoting mechanoreceptive cell growth and generating contact of the colls when research semence represents an armal-associated mucleic calls of the present semence represents an armal-associated mucleic calls of the present semence represents an armal-associated mucleic calls of the present semence represents an armal with a colls of the present semence represents an armal-associated mucleic calls of the present semence represents an armal-associated mucleic calls of the present semence represents an armal call associated mucleic calls of the present semence represents an armal-associated mucleic call of the present semence represents an armal-associated mucleic call of the present semence represents an armal-associated mucleic call of the present semence represents an armal-associated mucleic call of the present semence represents an armal-associated mucleic call of the present semence represents an armal call call of the present semence the p
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Best Local
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                                                                                                                                                                                                                                                                     AAF27273 standard;
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                                                                                                                                 Mouse atonal homologue 4A (Math4A) cDNA,
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                                                                                                                                   SEQ ID
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hearing impairment; vestibular effect; balance disorder; osteoarthritis; cellular proliferation; cerebellar granule neuron; gene therapy; mechanoreceptive cell growth; auditory; osteopathic; cytostatic;

Atonal; homologue; orthologue; atonal-associated protein; deafness;

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ARESULT 28
AAD47278
ID AAD47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein. They may particularly be used to treat an animal with a deficiency in cerebellar granule neurons or their precursors, and may also be used in promoting mechanoreceptive cell growth and generating hair cells. The present sequence represents an atonal-associated nucleic acid sequence referred to in the invention.

Note: The present sequence is not shown in the specification, but
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   WO200274946-A2
                                                              Homo sapiens
                                                                                                                        Human; insulin-secreting cell; neurogenin 3; ngn3; precursor stem cell; pancreatic exocrine cell; transplantation; RT-PCR; primer; ss.
                                                                                                                                                                                                                    Human RT-PCR upstream primer for neurogenin-3 DNA isolation.
                                                                                                                                                                                                                                                                                     24-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                              AAD47278 standard;
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19-JAN-2000; 2000US-0176993.
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                                                                                                                                                                                                                                                                                                                                                                                                              DNA;
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RESULT 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method for generating insulin-secreting cells (c) from precursor stem cells or adult pancreatic exocrine cells. The method (c) comprises exposing the precursor cells or exocrine cells to: a nucleic acid molecule encoding neurogenin 3 (ngm3) or NeuroD/beta2; or an (c) activator of ngm3 or NeuroD/beta2 gene expression, under conditions (c) effective to generate the insulin-generating cells from the precursor or (c) exocrine cells. The invention is useful in generating insulin-secreting (c) cells from precursor stem cells or adult pancreatic exocrine cells is (c) cuseful for generating glucose sensitive insulin secreting beta cells (s) cuseful for generating glucose sensitive insulin secreting beta cells (s) contable for transplantation, and for in situ development of insulin-correcting cells in a patient. The method is also useful for preventing compounds that prevent or activate beta (cells and for identifying compounds that prevent or activate beta (cell differentiation. The present sequence is human RT-PCR primer for isolation of neurogenin-3 DNA.
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Best Local :
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Serup P,
                                                                                                                                                                                                                              Human; insulin-secreting cell; neurogenin 3; ngn3; precursor stem cell; pancreatic exocrine cell; transplantation; RT-PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                 24-FEB-2003
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                                                                 26-FEB-2001;
                                                                                                26-FEB-2002; 2002WO-DK00130.
                                                                                                                                 26-SEP-2002
                                                                                                                                                                 WO200274946-A2
                                                                                                                                                                                                                                                                               Human RT-PCR forward primer for mouse ngn3 DNA isolation
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 Heimberg H, Gradwohl G;
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Pred. No.
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RESULT 30
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type 2
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                WPI; 2002-759853/82
P-PSDB; AAE29280.
                                                                                     German
                                                                                                                                                                                                                                                                                                                     WO200274045-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human neurogenin 1 (Ngn1) gene #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD46889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD46889 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 5B; Page 37; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-018804/01.
                                                                                                                                                                              20-MAR-2001; 2001US-0817360
                                                                                                                                                                                                                        20-MAR-2002; 2002WO-US11166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 differentiation. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      798 CCGGATGACGCCAAACTTACA 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                     SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcription factor; neuroendocrine basic helix-loop-helix; bHLH; diabetes mellitus; autoimmune destruction; type 1 diabetes;
                                                                                                                                UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCGGATGACGCCAAACTTACA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of mouse ngn3
                                                                                   Lin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP; 7 A; 7 C; 4 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    relates
                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                         /*tag=  a
/product= "Human Ngn1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapy; neurogenin 1; Ngn1; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to a method for generating insulin-secreting cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    °,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is human RT-PCR primer for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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RESULT 31
AAT74891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method for producing a mammalian islet cell. The method comprising introducing into a mammalian cell a nucleic acid molecule encoding an islet transcription factor for expression of the islet transcription factor in the cell and for production of islet cell phenotype in the cell. The islet transcription factor is a neuroendocrine basic helix-loop-helix (bHLH) transcription factor. The method is useful for treating type 2 diabetes mellitus and for replacing beta cells lost to autoimmune destruction in individuals with type 1 diabetes. The method is useful in cell therapy. The present sequence is human neurogenin 1
                                                                                                                                                             Nucleic acid encoding neurogenic differentiation polypeptide - useful e.g. in regulating neuronal, endocrine and gastrointest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neurogenic differentiation protein; NeuroD; neuroD3 gene; transcriptional activator; neuron; pancreas; gastrointestine; knock-out mouse; transgenic animal; cancer; diabetes; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human neurogenic differentiation protein (NeuroD3) DNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT74891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 714 BP; 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
                                                                              Claim 1; Page 64-65; 81pp; English.
                                                                                                                                                                                                                                               P-PSDB; AAW22440.
                                                                                                                                                                                                                                                                           WPI; 1997-272117/24.
                                                                                                                                                                                                                                                                                                                              Hollenberg SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT74891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9716548-A1
                                                                                                                                                                                                                                                                                                                                                                                   (HUTC-) HUTCHINSON CANCER RES (WEIN/) WEINTRAUB N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Ngn1) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; DNA; 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGCGCAACCGCATGCACAAC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGCGCAACCGCATGCACAAC 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neuroendocrine basic helix-loop-helix transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 94; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                              Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers 55..768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.4%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; 287
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                                                                                                                                                                                                                                                                                                                              Tapscott SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>;</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 T; 0
                                                                                                                                                                                                                                                                                                                                 Weintraub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   other;
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                                                                                                                                                                gastrointestinal
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Neurogenic differentiation (NeuroD) genes (AAT74887-94) and proteins (AAW22436-43) from human, mouse and frog have been identified,

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AAV42933
AAV42933
AAV42933
ID AAV42
XX 25-MA
DT 25-MA
DT 21-OC
XX DNA e
XX Basic
XX Class
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-MAY-1994;
02-NOV-1995;
30-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isolated and sequence. NeuroD polypeptides are tissue-specific basic-helix-loop-helix (bHLH) transcriptional activators involved in neuronal, endocrine and gastrointestinal development. They were discovered by expression cloning and screening assays designed to identify possible bHLH proteins capable of interacting with the protein product of the Drosophila daugherless gene. Novel neuroD2 and neuroD3 genes, related to neuroD1, have been identified. NeuroD noulclic acids can be used to produce NeuroD polypeptides, construction of test cell lines, as probes, in gene therapy, and to produce transgenic animals as models of disease.
The present sequence encodes a protein which is a member of the basic helix-loop-helix (bHLH) protein family, and is designated neuroD3. The bHLH genes are a family of genes associated with vertebrate neuronal, endocrinal and gastrointestinal development. The observed pattern of neuroD expression distinguishes subclasses of neuroectodermal tumours. The specification describes a method for the classification of human
                                                                                                                                                                                                                                                                        Classifying neuroectodermal tumours from expression pattern of basic-helix-loop-helix genes - especially for identifying medulla:blastoma and assessing its aggressiveness, specifically associated with expression of BHLH genes neuroD 1-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Basic helix-loop-helix; bHLH; neuroD; neuroectodermal tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1268 BP;
                                                                                                                                                                                                                  Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Olson JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUTC-) HUTCHINSON CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
21-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tapscott SJ;
                                                                                                                                                                                                               Columns 61-64; 43pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (updated)
(first en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human neuroD3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94US-0239238.
95US-0552142.
96WO-US17532.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  medulloblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/product= neuroD3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 A; 455 C; 344 G;
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein, which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 18;
6.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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RESULT 33
ABS56390
ID ABS56
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                               06-MAY-1994;
08-MAY-1995;
02-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; gene; ds; neuroD; basic-helix-loop-helix; bHLH; differentiation; neurone; endocrine; gastrointestine; development; transgenic; embryo; birth defect; spontaneous abortion; stem cell; cancer; neural growth factor; tumour; diagnostic; motor; sensory; traumatic neural injury; hearing; vision; brain; spinal cord; malabsorption syndrome; gastrointestinal dysmotility syndrome; Hirsh Prung's disease; therapeutic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neuroectodermal tumours. The method comprises measuring, in a tumour sample, expression of at least one basic bHLH gene and identifying the tumour subclass by matching expression to predetermined expression profiles for known subclasses. For classifying the tumour as a medulloblastoma, the bHLH gene detected is neuroD1 and neuroD3. The method is used to classify neuroectodermal tumours, and to identify medullablastoma and for prognosis of this as aggressive. (Updated on 25-MAR-2003 to correct PR field.)
                                                     New neurogenic differentiation gene, useful in gene therapy to correct traumatic neural injury that has resulted in loss of motor or sensory neural function and for constructing recombinant cell lines -
                                                                                                                                                                                                                                                                                                                                                               30-OCT-1996;
07-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human bHLH family neuroD3 genomic DNA, clone 20A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABS56390 standard; DNA; 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1268 BP; 245
                                                                                                                                                                                                                                                 Tapscott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6444463-B1
                                                                                                                                                                                                                                                                                                      (HUTC-) HUTCHINSON CANCER RES CENT FRED
                                                                                                                                                                                           2003-056678/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
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Similarity 100.0%;
                                                                                                                                                                    ABG72002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGCGCAACCGCATGCACAAC 375
                                                                                                                                                                                                                                                   ; LS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0499227.
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                                                                                                                                                                                                                                                                                                                                                          94US-0239238.
95WO-US05741.
95US-0552142.
96WO-US17532.
97US-0910973.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-US16417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "NeuroD3" 376..495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "HLH coding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                   that has resu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                °,
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; 344 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ,.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Claim 1; Column 61-64; 43pp; English

XAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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RESULT 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transformed host cells, nucleic acids and polypeptides are also useful for treating sites of traumatic neural injury where motor or sensory neural activity has been lost, e.g. hearing or vision loss and brain or spinal cord damage. The host cells find use in the treatment of malabsorption syndromes or gastrointestinal dysmotility syndromes (Hirsh Prung's Disease). The cell lines also find use in screening for candidate therapeutic agents capable of either substituting for neuron or correcting the cellular defect caused by a defective neuron. The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  correcting the cellular defect caused by a defective ne presented is the human neuroD3 genomic DNA, clone 20A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 implicated in the regulation of differentiation. NeuroD proteins are particularly involved in neuronal, endocrine and gastrointestinal development. The nucleic acid is useful for constructing recombinant cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    functionally active human neuroD3 polypeptide. NeuroD proteins represent a new family within the basic-helix-loop-helix (bHLH) family which are
                                                                                                                                                                                                                      30-OCT-1996;
                                                                                                                                                                                                                                                                                     09-MAY-1997.
                                                                                                                                                                                                                                                                                                                                                   WO9716548-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transcriptional activator; neuron; pancreas;
knock-out mouse; transgenic animal; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neurogenic differentiation protein; NeuroD; neuroD2 transcriptional activator; neuron; pancreas; gastroi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human neurogenic differentiation protein (NeuroD2) DNA clone 14B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT74890 standard; DNA; 1535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1268 BP; 245
Hollenberg SM,
                                                           (HUTC-) HUTCHINSON CANCER RES (WEIN/) WEINTRAUB N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention discloses an isolated nucleic acid molecule which encodes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              732 GAGCGCAACCGCATGCACAAC 752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                           95US-0552142
                                                                                                                                                                                                                      96WO-US17532
Lee
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                  D)
Tapscott SJ,
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Pred. No.
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                                                                                               CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                               FRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer; diabetes; gene therapy;
Weintraub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gastrointestine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1268;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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ARAV42931
ID AAV42931
ID AAV42931
AC AAV42
XX AAV42
XX 25-MA
DT 25-MA
DT 21-OC
XX DNA e
XX Basic
KW Class
XX Homo
XX Homo
XX Class
XX Homo
XX Homo
XX O7-AU
PF O7-AU
XX O7-AU
PR 06-MA
PR 02-NC
XX HOTC
XX O18on
XX WPI;
DR P-PSD
PT Class
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                           06-MAY-1994;
02-NOV-1995;
30-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NeuroD nucleic acids can be used to produce NeuroD polypeptides, construction of test cell lines, as probes, in gene therapy, and to produce transgenic animals as models of disease.
Classifying neuroectodermal tumours from expression pattern basic-helix-loop-helix genes - especially for identifying
                                           P-PSDB; AAW71015
                                                          WPI; 1998-466661/40
                                                                                      Olson JM,
                                                                                                                                                                                                     07-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                          Basic helix-loop-helix; bHLH; neuroD; neuroectodermal tumour; classification; medulloblastoma; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2003
21-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV42931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1535 BP; 250 A; 559 C; 476 G; 244 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    discovered by expression cloning and screening assays designed to identify possible bHLH proteins capable interacting with the protein product of the Drosophila daugherless gene. Novel neuronal and neuron3 genes, related to neuron1, have been identified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              basic-helix-loop-helix (bHLH) transcriptional activators involved
in neuronal, endocrine and gastrointestinal development. They wen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding neurogenic differentiation polypeptide - useful e.g. in regulating neuronal, endocrine and gastrointestinal
                                                                                                                                                                                                                                  18-AUG-1998
                                                                                                                                                                                                                                                             US5795723-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV42931 standard; DNA; 1535 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neurogenic differentiation (NeuroD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 61-62; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAW22439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-272117/24.
                                                                                                                (HUTC-) HUTCHINSON CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isolated and sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AAW22436-43)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        729 CGGGAGCGCAACCGCATGCAC 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGGGAGCGCAACCGCATGCAC 459
                                                                                      Tapscott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      human neuroD2 protein, which is a bHLH protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from human,
                                                                                                                                            94US-0239238.
95US-0552142.
96WO-US17532.
                                                                                                                                                                                                     97US-0910973
                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 55..1194
                                                                                                                                                                                                                                                                                         /product= neuroD2
                                                                                                                                                                                                                                                                                                        *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NeuroD polypeptides are tissue-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mouse and
                                                                                                                   CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genes (AAT74887-94) and p
frog have been identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              They were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neuroD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                         05-AUG-1998;
06-MAY-1994;
08-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes a protein which is a member of the basic helix-loop-helix (bHLH) protein family, and is designated neuroD2. The bHLH genes are a family of genes associated with vertebrate neuronal, endocrinal and gastrointestinal development. The observed pattern of neuroD expression distinguishes subclasses of neuroectodermal tumours. The specification describes a method for the classification of human neuroectodermal tumours. The method comprises measuring, in a tumour sample, expression of at least one basic bHLH gene and identifying the
                                                                                                                                                                                                                                                                                                                                                                        Human; gene; ds; neuroD3; neuroD; basic-helix-loop-helix; bHLH; differentiation; neurone; endocrine; gastrointestine; development; transgenic; embryo; birth defect; spontaneous abortion; stem cell; cancer; neural growth factor; tumour; diagnostic; motor; sensory; traumatic neural injury; hearing; vision; brain; spinal cord; malabsorption syndrome; gastrointestinal dysmotility syndrome; Hirsh Prung's disease; therapeutic; neuroD2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        medulla:blastoma and assessing its aggressiveness, specifically associated with expression of BHLH genes neuroD 1-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            medulloblastoma, the bHLH gene detected is neuroD1 and neuroD3. The method is used to classify neuroectodermal tumours, and to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumour subclass by matching expression to predetermined expression profiles for known subclasses. For classifying the tumour as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1535 BP;
                                             02-NOV-1995;
30-OCT-1996;
                                                                                                                                    07-FEB-2000;
                                                                                                                                                                                             US6444463-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human bHLH family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABS56389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABS56389 standard; DNA; 1535 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  medullablastoma and
 (HUTC-)
                                                                                                                                                                                                                                                       _feature
                                                                                                                                                                                                                                                                                                                                               sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   439
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 HUTCHINSON CANCER RES CENT FRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGGAGCGCAACCGCATGCAC 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGGGAGCGCAACCGCATGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coma and for prognosis of this as aggressive. 25-MAR-2003 to correct PR field.)
                                                                                                                                     2000US-0499227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                           95US-0552142.
96WO-US17532.
97US-0910973.
                                                                          94US-0239238.
95WO-US05741.
                                                                                                        98WO-US16417.
                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                        463..582
                                                                                                                                                                                                                                                                                                  55..1194
                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                     /product= "NeuroD2"
                                                                                                                                                                                                                         note = "HLH coding domain"
                                                                                                                                                                                                                                                                                    *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250 A; 559 C; 476 G; 244 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neuroD2 genomic DNA, clone 14B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.4%;
                                                                                                                                                                                                                                                                                      മ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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RESULT 37
AAA62681
ID AAA62
XX AA62
XX AA62
XX AA62
XX Lumar
XX Humar
XX Humar
XX Humar
XX neurc
KW Alzhe
XX Homo
XX Homo
XX Homo
XX Homo
XX Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            뭕
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       development. The nucleic acid is useful for constructing recombinant cell clines, transgenic embryos and animals and for quantifying the level of cexpression of neuroD in a cell. Birth defects and spontaneous abortions may result from expression of an abnormal neuroD protein. The complete embryosic neuronal stem cells under conditions mimicking those that are active in development and cancer. The resultant cell lines of groliferating embryonic neuronal stem cells under conditions mimicking those that are active in development and cancer. The resultant cell lines of find use as sources of novel neural growth factors, in assays for cell dentifying novel neuronal growth factors, in assays for continuous, for producing antibodies useful in diagnostic assays and for screening for compounds capable of minimal differentiation in neural culturers, for producing antibodies useful in diagnostic assays and for screening for compounds capable of modulating the activity of neuron. Transformed host cells, nucleic acids and polypeptides are also useful for treating sites of traumatic neural injury where motor or sensory companies of the cells find use in the treatment of malabsorption syndromes or gastrointestinal dysmotility syndromes (Hirsh crecital in the cell lines also find use in screening for candidate thoracters in the cell lines also find use in screening for candidate correcting the cellular defect caused by a defective neuron. The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New neurogenic differentiation gene, useful in gene therapy to traumatic neural injury that has resulted in loss of motor or seneral function and for constructing recombinant cell lines -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-056678/05
                                                                                                                                                                         epidermal cell transdifferentiation; gene therapy; cerebroproneuroprotective; brain injury; spinal cord injury; stroke; neurodegenerative disease; Parkinson's disease; Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention discloses an isolated nucleic acid molecule which encodes
                                                                                                                                                          Alzheimer's disease;
                                                                                                                                                                                                                                      Human; NeuroD2; neurogenic basic helix-loop-helix protein;
                                                                                                                                                                                                                                                                            Human NeuroD2
                                                                                                                                                                                                                                                                                                                 29-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                            AAA62681 standard; DNA; 1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           implicated in the regulation of differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             functionally active human neuroD3 polypeptide. NeuroD proteins represent a new family within the basic-helix-loop-helix (bHLH) family which are
                                                                                                                  sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              439 CGGGAGCGCAACCGCATGCAC 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGGAGCGCAACCGCATGCAC 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is the human neuroD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Column
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                          gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP; 250 A;
                                                         Location/Qualifiers 58..1206
                                      *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57-60; 43pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.4%;
100.0%;
                                                                                                                                                          neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     559 C; 476 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 21;
Pred. No.
                                                                                                                                                            cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                        generation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6. B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone 14B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                            ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NeuroD proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                               cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sensory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            correct
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/product= "NeuroD2 protein"

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RESULT 38
AAD46888
ID AAD46
XX AAD46
XX AAD46
XX Human
XX Human
XX Human
XX Human
XX Homo
XX Eype
XW Lype
XW MO201
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Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein (Neuron2) gene from Genbank. It was used to provide sequence information for the cloning of Neuron2 cDNA, which was used to transfect cultured epidermal cells. This was part of a novel method for transdifferentiating an epidermal basal cell into a cell having the morphological, physiological and/or immunological features of a viable neuronal cell. The method is useful for screening new drugs for treating a nervous system disorder, or for isolating a novel nerve growth factor. The transdifferentiated cell is useful in both cell and gene therapies aimed at alleviating various neurological disorders. The cell or gene therapy approach involves the use of autologous transplantation or grafting of the newly created neuronal cells as treatment for brain or spinal cord injury, stroke and neurodegenerative diseases (e.g. Parkinson's disease, Huntington's disease or Alzheimer's
                                                                                                                                                                                             Human;
type 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Converting epidermal cells growth factors or for gene and transfecting with vectors.
                                                                                                                                                                                                                                             Human neurogenin 1 (Ngn1) gene #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example
                                                                                                                                                                           Human; transcription factor; neuroendocrine basic helix-loop-helix; bHLH, type 2 diabetes mellitus; autoimmune destruction; type 1 diabetes; islet cell; cell therapy; neurogenin 1; Ngn1; gene; ds.
                                                                                                                                                                                                                                                                                                                                              AAD46888 standard; DNA; 1665 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transcription factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JUL-2000.
                              WO200274045-A2
                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                               27-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is the human neurogenic basic helix-loop-helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Levesque MF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CEDA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US6087168-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000-498200/44.
                                                                                                                                                                                                                                                                                                                                                                                                                             442
                                                                                                                                                                                                                                                                                                                                                                                                                                                            729 CGGGAGCGCAACCGCATGCAC 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Column 19-22; 27pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CEDARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB14347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1550 BP; 250
                                                                                                                                                                                                                                                                                                                                                                                                                             CGGGAGCGCAACCGCATGCAC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                           (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neuman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SINAI MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9908-0234332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0234332
                                                                                                              Location/Qualifiers
                                                              'product= "Human Ngn1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cells into neurons, useful for isolating nerve gene therapy, comprises dedifferentiating cel vectors with a cDNA coding neurogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; 569 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 21; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             486 G; 243 T; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cells
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RESULT 39
AAL04043/c
ID AAL040
XX AAL040
XX AAL040
XX Human
XX Human
XX Homo 8
XX Homo 8
YX Cancer
XX Cancer
XX Homo 8
YX Homo 9
YX 17-JAN
YX 11-JAN
YX 11-J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                           16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
  28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method for producing a mammalian islet cell. The method comprising introducing into a mammalian cell a nucleic acid molecule encoding an islet transcription factor for expression of the islet transcription factor in the cell and for production of islet cell phenotype in the cell. The islet transcription factor is a neuroendocrine basic helix-loop-helix (bHHH) transcription factor. The method is useful for treating type 2 diabetes mellitus and for replacing beta cells lost to autoimmune destruction in individuals with type 1 diabetes. The method is useful in cell therapy. The present sequence is human neurogenin 1
                                                                                                                                                                                                                                                                       31-JAN-2000;
04-FEB-2000;
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02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; reproductive system related antigen; reproductive system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human reproductive system related antigen DNA SEQ ID NO: 6731.
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2000US-0216880 2000US-0217487

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                                                 The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
                                Sequence 2776 BP; 631 A; 851
                                                                                                                      Disclosure;
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1.4%;
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Score 21; DB 22;
Pred. No. 6.3;
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                                C; 749 G; 545 T; 0 other;
                                                                                                                      Sequence Listing; English.
           Length 2776;
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3-0235834 5-0236327 5-0236387 5-0236368 5-0236368 5-0236360 5-0237038 5-0237038 5-0237038 5-0237038 5-0237039

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3-0234998. 3-0235484. 2000US-0231244. 2000US-0231413. 2000US-0231414. 2000US-0229345. 2000US-0229509. 2000US-0229513.

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3-0230438. 3-0231242. 2000US-0227009. 2000US-0228924. 2000US-0229287.

PR 08-SEE PR 08-SEE PR 14-SEE PR 21-SEE PR 21-SEE PR 22-SEE PR 21-NO\ PR 21-	PR 08-SEP-2000; 2000US-PR 08-SEP-2000; 2000US-PR 08-SEP-2000; 2000US-PR 08-SEP-2000; 2000US-PR 08-SEP-2000; 2000US-PR 14-SEP-2000; 2000US-PR 25-SEP-2000; 2000US	18-AUG-2000; 2000US 22-AUG-2000; 2000US 22-AUG-2000; 2000US 22-AUG-2000; 2000US 23-AUG-2000; 2000US 30-AUG-2000; 2000US 01-SEP-2000; 2000US	TILL-2000; 2000US	17-JAN-2001; 2001WO- 31-JAN-2000; 2000US- 04-FEB-2000; 2000US- 24-FEB-2000; 2000US- 16-MAR-2000; 2000US- 17-MAR-2000; 2000US- 18-APR-2000; 2000US- 19-MAY-2000; 2000US- 19-MAY-2000; 2000US- 07-JUN-2000; 2000US- 30-JUN-2000; 2000US-	RESULT 40 AAL04045/c ID AAL04045 standard; DNA; 2776 BP. XX AC AAL04045; XX PT 21-NOV-2001 (first entry) XX DE Human reproductive system related antigen DNA SEQ ID NO: 6733. XX KW Human; reproductive system related antigen; reproductive system disorder; XX Cancer; gene therapy; ds. XX CANCER; Gene therapy; ds. XX NOS Homo sapiens. XX NOS Homo sapiens. XX NOCO0155320-A2. XX PD 02-AUG-2001.	Qy 1112 AACAGGCCCTGGGCGGTGGGC 1132
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                                                                                                                                                                                                                                                                      Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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2000US-0225759
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2000US-0198123
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                                                                                        WPI;
AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
                                                  useful for metastasis
                                                         Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                              Disclosure; SEQ ID NO 23287; 3071pp + Sequence Listing; English.
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                                                                                        2001-483426/52.
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                                                                                                                              HUMAN
                                                    preventing,
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2000US-0251856.
2000US-0251868.
2000US-0251869.
2000US-0251869.
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2000US-0240960.
2000US-0241221.
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2000US-0249217
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2000US-0249212
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2000US-0246611.
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2000US-0244617
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2000US-0249210
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RESULT 42
AAK68476
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Best Local
                                   30-JUN-2000

07-JUL-2000

07-JUL-2000

11-JUL-2000

11-JUL-2000

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26-JUL-2000

26-JUL-2000

14-AUG-2000

14-AUG-2000

14-AUG-2000

14-AUG-2000

14-AUG-2000
                                                                                                                                                                                                                                    02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I) additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703
                                                                                                                                                                                                         07-JUN-2000;
28-JUN-2000;
                                                                                                                                                                                                                                                                                                                                      31-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic; gene therapy; vaccine; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immune/haematopoietic antigen genomic sequence
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                                                                                                                                                                                                                                                                                                                                                                                              09-AUG-2001
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Similarity 100.0%; Pred. No.
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                                    2000US-0224519.
2000US-0225213.
2000US-0225214.
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2000US-0217496
2000US-0218290
2000US-0220963
2000US-0220964
2000US-0224518
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2000US-0198123.
2000US-0205515.
2000US-0209467.
2000US-0214886.
2000US-0215135.
2000US-0216647.
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2000US-0189874.
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2000US-0225267
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2000US-0184664.
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6.3;
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2000US-0226681

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CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cattivity, and can be used in gene therapy and vaccine production. (I) corrections and polynucleotides may be used in the prevention diagnosis and treatment of diseases associated with inappropriate (I) expression. For cexample, they may be used to treat disorders associated with decreased cexpression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) collines at the section of the secreted (I), by inserting the mucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, and cancer metastases of haematopoietic-derived cells. AAK64703 cc cancers and cancer metastases of haematopoietic antigen genomic cto AAK87694 represent human immune/haematopoietic antigen genomic crepresent sequences used in the exemplification of the present invention.
Query Match
Best Local Similarity
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01-DEC-2000
01-DEC-2000
05-DEC-2000
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                                             Sequence 2776 BP;
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CA
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2000US-0250360.
2000US-0250391.
2000US-0251030.
2000US-0251030.
2000US-0251479.
2000US-0251479.
2000US-0251866.
2000US-0251866.
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2000US-0249265.
2000US-0249297.
2000US-0249299.
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2000US-0249215

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2000US-0249248

2000US-0249244
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2000US-0246532.
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                                              545 A; 747 C; 853 G; 631 T; 0 other;
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1.4%; Score 21; DB 22; 100.0%; Pred. No. 6.3;
                                                                                                                                                                                                                                                                                                                                                                                                       human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and
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              Length 2776;
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2000US-0234223. 2000US-0234274. 2000US-0234997.

2000US-0233063. 2000US-0233064. 2000US-0233065. 2000US-0232398. 2000US-0232399. 2000US-0232400. 2000US-0231413. 2000US-0231414. 2000US-0232080. 2000US-0232081.

2000US-0236327. 2000US-0236367. 2000US-0236368. 2000US-0236369. 2000US-0236370.

2000US-0234998 2000US-0235484 2000US-0235834 2000US-0235836 14-AUG-2000
114-AUG-2000
12-AUG-2000
22-AUG-2000
23-AUG-2000
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29-SEP-2000
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2000US-0239935 2000US-0239937

2000US-0241787. 2000US-0241808. 2000US-0241809. 2000US-0241826. 2000US-0244617.

2000US-0246474

2000US-0246475. 2000US-0246476. 2000US-0246477. 2000US-0246478. 2000US-0246523. 2000US-0246524. 2000US-0246524. 2000US-0246526. 2000US-0246526.

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RESULT 43
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                                                 The invention describes an isolated murine polynucleotide (I) comprising CC a contiguous stretch of at least 60 nucleotides of one of 265-677 CC nucleotide 891 OMNIBANK gene trapped sequences (GTSS) (S), given in the CC genomic analysis and in the discovery and development of new therapeutic CC and diagnostic agents and methods. (I) is useful in functional CC genomic analysis and in the discovery and development of new therapeutic CC and diagnostic agents and methods. (I) is useful for identifying the CC coding regions of the murine genome, to isolate cDNAs, genomic clones, CC paralogues, or orthologues that are capable of hybridising to one or more CC figures, or orthologues that are capable of proteins, or other CC ligands, that are capable of binding an amino acid sequence encoded by CC an oligonucleotide or polynucleotide sequence in at least one of the TS CC sequences. (I) is useful in addressable arrays, such as gene chips, to CC identify and characterise temporal and tissue specific gene expression, CC identify the gene of interest from many sources and for genetic CC manipulations such as antisense inhibition and gene targeting. Decreasing CC the level of expression of (I) and/or down regulating the activity of CC peptides or proteins encoded by (I) is useful for treating development CC and cell differentiation disorders, aging, cancer, autoimune disease, CC lupus, inflammatory disorders, skin disorders and collect with the content of the collect of the colle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel murine polynucleotides that individually identify novel genes into which a retroviral gene trap vector has integrated, useful in genomic analysis and in discovery, development of therapeutic and
                                        lupus, int.
disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 57; 296pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnostic agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention describes
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                                      sequence
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                                      degenerative isolated using
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CC This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic CC DNA that contains the target C is amplified to form a labeled amplicon. CC The amplicon is hybridised to two classes, each with at least one CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers CC and the degree of hybridisation to both classes is determined from the CC label on the amplicon. From the ratio of labels hybridised to the two C1 is used: (i) for diagnosis and/or prognosis of side effects of CC is used: (i) for diagnosis and/or prognosis of side effects of the central nervous, cardiovascular, gastrointestinal and respiratory cosystems etc., particularly by detecting mutations or single nucleotide CC types and for investigating cell differentiation. The method allows the CC types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously.
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ABQ49522/c
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                            ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate method for determining the degree of cytosine methylation described ithe disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                               Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide
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                                                                                                                                                                                                                                                                                                                                                                  Claim 12; 56pp + Sequence Listing; 56pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-371829/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-SEP-2000;
05-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      drug; side effect; cancer; central nervous system; cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JUL-2002
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2000DE-1044543
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Query Match

Sequence

592

81

A; 59 C;

251

T; 0 other

1.48;

Score 20; 201 G;

DB 24; Length 592;

RESULT 45 ABQ49523 밁 á This invention describes a novel method for determining the degree of cc methylation of a particular cytosine in a motif 5'-CpG-3', present in a cc genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. Cc member, of oligonuclotides and/or peptide-nucleic acid (PNA) oligomers cc member, of oligonuclotides and/or peptide-nucleic acid (PNA) oligomers cc and the degree of hybridisation to both classes is determined from the classes of oligomers, the degree of methylation is calculated. The method is used: (1) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders cf the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide colymorphisms (SNP's); and (ii) for differentiation. The method allows the cmethylation status of many C residues to be determined simultaneously. Cc MB013410-AB054121 represent genomic DNA sequences used to illustrate the cmethod for determining the degree of cytosine methylation described in the disclosure of the invention. Query Match Best Local Similarity Matches Best Local Similarity 100.0%; Pred. No. 21; Matches Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds. Sequence 592 BP; Claim 12; 56pp + Sequence Listing; 56pp; German. WPI; 2002-371829/40. Olek A, 01-SEP-2000; 2000DE-1043826 05-SEP-2000; 2000DE-1044543 01-SEP-2001; 2001WO-EP10074. 07-MAR-2002. WO200218632-A2. Homo sapiens. Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; Oligonucleotide for detecting cytosine methylation SEQ ID 12-JUL-2002 (first entry) ABQ49523; ABQ49523 standard; DNA; 592 BP (EPIG-) EPIGENOMICS AG. 834 CGCTTCGCCCACAACTACAT 853 68 CGCTTCGCCCACAACTACAT 49 20; Piepenbrock C, Conservative 1.4%; Score 20; DB 24; Length 592; ilarity 100.0%; Pred. No. 21; Conservative 0; Mismatches 0; Indels 251 A; 201 C; 59 G; 81 Berlin ٥, Mismatches ζ, Guetig D; T; 0 other; o ; Indels NO 36114. 0 0; Gaps Gaps 0 0

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Qy 834 CGCTTCGCCCACAACTACAT 853
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Db 525 CGCTTCGCCCACAACTACAT 544
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Search completed: January 26, 2004, 22:22:39 Job time : 428 secs

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Result
No.
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   Score
                                                                                                                                                                                                                                                                                                                                       Published Applications NA:*

1: /cgn2=6/ptodata/1/pubpna/US07 PUBCOMB.seq:*

2: /cgn2-6/ptodata/1/pubpna/US06 NEW PUB.seq:*

3: /cgn2-6/ptodata/1/pubpna/US06 NEW PUB.seq:*

4: /cgn2-6/ptodata/1/pubpna/US07 NEW PUB.seq:*

5: /cgn2-6/ptodata/1/pubpna/PCTUS PUBCOMB.seq:*

6: /cgn2-6/ptodata/1/pubpna/US07 NEW PUB.seq:*

6: /cgn2-6/ptodata/1/pubpna/US08 NEW PUB.seq:*

7: /cgn2-6/ptodata/1/pubpna/US08 PUBCOMB.seq:*

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9: /cgn2-6/ptodata/1/pubpna/US09E PUBCOMB.seq:*

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11: /cgn2-6/ptodata/1/pubpna/US09E PUBCOMB.seq:*

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13: /cgn2-6/ptodata/1/pubpna/US09 NEW PUB.seq:*

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15: /cgn2-6/ptodata/1/pubpna/US09 NEW PUB.seq:*

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18: /cgn2-6/ptodata/1/pubpna/US09 NEW PUB.seq:*

19: /cgn2-6/ptodata/1/pubpna/US09 NEW PUB.seq:*
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                                                                                                                                                                                                                                                                                                                 cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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                                                                                                          SUMMARIES
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9417.792 Million cell updates/sec
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-10-027-632-2	-10-029-386	US-10-029-386-2219	o	US-10-027-632-184196	US-10-242-535A-3008	US-09-764-891-8888	-891-8	US-10-027-632-111284	US-10-027-632-111283	US-10-027-632-111282	US-10-027-632-111284	US-10-027-632-111283	US-10-027-632-111282	-842A-103	US-09-938-842A-1036	US-10-027-632-157510	US-10-027-632-157510	US-10-027-632-276355	US-10-027-632-276355	US-10-260-238-5886	83-590-		US-09-728-445-108	64-891-	US-09-764-891-6731	US-10-027-632-129768	US-10-027-632-129767	US-10-027-632-129768	TO-021-036-120-01
(D		Sequence 2219	æ	Sequence 1841	æ	ø		Sequence 1112			Sequence 111284	Sequence 1112	Sequence 1112	Sequence 1036	æ	Sequence 157510	Sequence 1575		Sequence 2763!	æ			æ			Sequence 129768	Φ		a
140,	•	9, Ap		196,	•	•	•	284,	283,	282,	284,	283,	82	•	6, Ap	510,	510,	355,	55	•		98, A		•	l, Ap	768,	767,	768,	

ALIGNMENTS

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GENERAL INFORMATION:

APPLICANT: ZOGHBI, HUDA Y.

APPLICANT: ZOGHBI, HUDA Y.

APPLICANT: YANG, OI

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN TITLE OF INVENTION: ATONAL ASSOCIATED SEQUENCE FOR DEAFNESS,

TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION FILE REFERENCE: PO1899US4

CURRENT PAPLICATION NUMBER: US/10/004,717

CURRENT PAPLICATION NUMBER: US/10/004,717

PRIOR APPLICATION NUMBER: 09/585,645

PRIOR APPLICATION NUMBER: 60/176,993

PRIOR PILING DATE: 2000-06-01

PRIOR PILING DATE: 2000-01-19

PRIOR PILING DATE: 1099-06-01

PRIOR PILING DATE: 1099-06-01

PRIOR FILING DATE: 1099-06-01

PRIOR FILING DATE: 1099-06-01
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                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 4
LENGTH: 645
                                                                                                                                                                                                                Query Match 6.3%; Score 92; DB 14; 1
Best Local Similarity 100.0%; Pred. No. 3.9e-37;
Matches 92; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/10004717 Publication No. US20020192665A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 69
                               822 ATCGAGACCCTGCGCTTCGCCCACAACTACAT 853
                                                                                                          304 GCGCTGGATGCGCTGCGCGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAG 363
                                                                                                                                          762 GCGCTGGATGCGCTGCGCGGTGTCCTGCCCACCTTCCCCGGATGACGCCAAACTTACAAAG 821
364 ATCGAGACCCTGCGCTTCGCCCACAACTACAT 395
                                                                                                                                                                                                                                                                      Length 645;
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US-10-004-717-24

Sequence 24, Application US/10004717
Publication No. US20020192665A1
GENERAL INFORMATION:

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; LENGTH: 861
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-004-717-24
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                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Mus musculus
US-09-817-360-3
                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: German, Michael S.
APPLICANT: Lin, Joseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                              Query Match
Best Local Similarity
Matches 92; Conserv
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CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/585,645
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: 60/176,993
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 2000-01-19
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APPLICANT: YANG, QI

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF
TITLE OF INVENTION: ATONAL ASSOCIATED SEQUENCE FOR DEARNESS,
TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION
FILE REFERENCE: P01899US4
                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/817,360
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/535,145
PRIOR FILING DATE: 2000-03-24
                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/128,180 PRIOR FILING DATE: 1999-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PRODUCTION OF PANCREATIC ISLET CELLS TITLE OF INVENTION: AND DELIVERY OF INSULIN FILE REFERENCE: UCSF-129CIP
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SOFTWARE: PatentIn Ver. 2.1
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1396 GCGCTGGATGCGCTGCGCGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAG 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       822 ATCGAGACCCTGCGCTTCGCCCACAACTACAT 853
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                                            762
                                            GCGCTGGATGCGCTGCGCGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAG
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                                                                                              Conservative 0;
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                                                                                                                     6.3%; Score 92; DB 9; Locore 100.0%; Pred. No. 3.5e-37;
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                                                                                                Mismatches
                                                                                                                                               Length 1861;
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                                                                                              Gaps
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US-09-908-975-4140
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                                                                                  ; ORGANISM: Mus musculus 
US-09-908-975-30269
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TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS /
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
150CTUR AS 140
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Matches
                                                                                                                         SEQ ID NO 30269
LENGTH: 65
TYPE: DNA
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                                         Query Match
                                                                                                                                                                                                                         TITLE OF INVENTION: OLICONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REFERENCE: 3668-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR PILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR PILING DATE: 2000-07-28
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APPLICANT: WASSERMAN,
                                                                                                                                                                                  PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SHOSHAN, APPLICANT: WASSERM
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Local Similarity 100.0%; hes 35; Conservative
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nes 36; Conservative 0;
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: MINTZ, Eli
: MINTZ, Liat
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MINTZ, Liat
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2.4%; Score 35; DB 13;
100.0%; Pred. No. 1.9e-0;
ive 0; Mismatches (
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100.0%; Pred. No. 5.1
ive 0; Mismatches
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hes 0;
  1.9e-07;
hes 0;
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RESULT 8
US-08-722-570-13
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LENGTH: 5340
TYPE: DNA
ORGANISM: Homo Sapiens
Sequence 13, Application US/08722570
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Best Local (
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CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/535,145
PRIOR FILING DATE: 2000-03-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kaia Palm
                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Probe
                                                                                                                                                                                                                                                                                                                                                                                    ENGTH: 26
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mes 32; Conserv
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26; Conservative (
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100.0%; Pred. No. 4.5e-06;
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                                                                                                                                                                                                            Score 26; pred. No.
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                                                                                                                                                                                                            DB 11; Length 26; 0.01;
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TELEFAX: (415)...
TELEFAX: 910 277299
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
LENGTH: 738 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-004-717-20
                                                             PRIOR APPLICATION NUMBER: 60/137,060
PRIOR ETILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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Publication No. US20020192665A1
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                                                                                                                                                                             TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF INTITLE OF INVENTION: ATONAL ASSOCIATED SEQUENCE FOR DEAFNESS,
TITLE OF INVENTION: OSTEDARTHRITIS, AND ABNORMAL CELL PROLIFERATION
FILE REFERENCE: P01899US4
CURRENT APPLICATION NUMBER: US/10/004,717
CURRENT APPLICATION NUMBER: US/10/004,717
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/585,645
PRIOR PILING DATE: 2000-06-01
PRIOR PILING DATE: 2000-01-19
PRIOR PILING DATE: 2000-01-19
PRIOR FILING DATE: 2000-01-19
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APPLICANT: Anderson,
APPLICANT: Ma, Qiufu
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ZOGHBI, HI APPLICANT: YANG, QI
ORGANISM: chicken
                      LENGTH: 790
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,570
FILING DATE: 27-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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les 23; Conservative (
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CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 GAGCGCAACCGCATGCACAACCT 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUDA Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEUROGENIN
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100.0%; Pred. No.
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; TYPE: DNA
; ORGANISM: Mus musculus
US-10-004-717-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-004-717-6
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Publication No. US20020192665A1
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Best Local S
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 30, Application US/10004717 Publication No. US20020192665A1
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                                                                                   SOFTWARE: PatentIn
SEQ ID NO 6
                                                                                                                                                                                                                                                                        APPLICANT: ZOGHBI, HUDA Y.

APPLICANT: YANG, QI
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF
TITLE OF INVENTION: ATONAL ASSOCIATED SEQUENCE FOR DEAFNESS,
TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION
FILE REFERENCE: PO1899US4
CURRENT APPLICATION NUMBER: US/10/004,717
CURRENT FILING DATE: 2002-08-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: 60/137,060
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ZOGHBI, HUDA Y.

APPLICANT: YANG, QI

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF

TITLE OF INVENTION: ATONAL ASSOCIATED SEQUENCE FOR DEAFNESS,

TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/585,645
PRIOR FILING DATE: 2000-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: P01899US4
CURRENT APPLICATION NUMBER: US/10/004,717
CURRENT FILING DATE: 2002-08-16
                                                                                                                                NUMBER OF SEQ ID NOS: 69
                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/137,060 PRIOR FILING DATE: 1999-06-01
                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/176,993 PRIOR FILING DATE: 2000-01-19
                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 09/585,645
PRIOR FILING DATE: 2000-06-01
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                                                               LENGTH: 1412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    742 GAGCGCAACCGCATGCACAACCT 764
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ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 14; Length 1385; 0.25;
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RESULT 12
US-10-004-717-37
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                                                                                        ; ORGANISM: Homo Sapien US-10-090-011-1
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Best Local S
Matches 23
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Best Local Similarity
Matches 23; Conserv
                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 21
TYPE: DNA
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LENGTH: 14
                                            Query Match
                                                                                                                                                                                                                   APPLICANT: Serup, Palle
APPLICANT: Heimberg, Harry
APPLICANT: Heimberg, Harry
APPLICANT: Gradwohl Gerard
TITLE OF INVENTION: Methods For Generating Insulin-Secreting
TITLE OF INVENTION: Cells Suitable for Transplantation
FILE REFERENCE: 6246.200-US
CURRENT APPLICATION NUMBER: US/10/090,011
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: US 60/271,474
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 70
ROTHWARE PARTS OF WARREN OF SEQ ID NOS: 70
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APPLICANT: YANG, QI
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF J
TITLE OF INVENTION: ATONAL ASSOCIATED SEQUENCE FOR DEAFWESS,
TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION
FILE REFERENCE: PO1899US4
CURRENT FAPLICATION NUMBER: US/10/004,717
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 60/136,645
PRIOR PILING DATE: 2000-06-01
PRIOR PILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: 60/137,060
PRIOR EPILING DATE: 2000-01-01
PRIOR APPLICATION NUMBER: 60/137,060
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y Match 1.4%; Score 21; DB 15; Length 21;
Local Similarity 100.0%; Pred. No. 4.1;
hes 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                  DNA
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100.0%; Pred. No. 0.
Live 0; Mismatches
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. 0.24;
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460 TGGCGCCTCATCCCTTGGATG 480

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SOFTWARE: FASTSEQ for Windows Version 4.0; SEQ ID NO 49
LENGTH: 21
TYPE: DNA
ORGANISM: Homo Sapien
US-10-090-011-49
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US-10-090-011-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 8222
LENGTH 1-1
                                                                                          Query Match
Best Local
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                                                                         Matches
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APPLICANT: Heimberg, Harry
APPLICANT: Gradwohl Gerard
TITLE OF INVENTION: Methods For Generating Insulin-Secreting
TITLE OF INVENTION: Cells Suitable for Transplantation
FILE REFERENCE: 6246.200-US
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: US/10/090,011
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: US 60/271,474
PRIOR FILING DATE: 2001-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
                                                                                                                                                                                   OTHER INFORMATION: MAP TO CHR16.3

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 67

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 64

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 9.8

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 41

OTHER INFORMATION: EST HUMAN HIT: BG166801.1, EVALUE 0.00e+00

OTHER INFORMATION: NT HIT: G114779902, EVALUE 3.00e-95

OTHER INFORMATION: SWISSPROT HIT: P25444, EVALUE 8.00e-58
                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH: 576
1112 AACAGGCCCTGGGCGGTGGGC 1132
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                                                                                             Similarity
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                                                               1.4%; Score 21; DB 13; Length 576; ilarity 100.0%; Pred. No. 2.9; Conservative 0; Mismatches 0; Indels
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tive 0; Mismatches
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Db 29 AACAGGCCCTGGGCGGTGGGC 49

Search completed: January 29, 2004, 22:30:14 Job time : 568 secs

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ALIGNMENTS

	TITLE JOURNAL COMMENT	REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 AZ296526/c LOCUS DEFINITION
Department of Bukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: szhao@tigr.org Clones are derived from the mouse BAC library RPCI-23. For BAC	Mouse BAC End Sequences from Library RPCI-23 Mouse BAC End Sequences from Library RPCI-23 Unpublished Other_GSSs: RPCI-23-160G18.TJ Contact: Shaying Zhao	<pre>Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 593) Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser C.M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.</pre>	, genomic survey se AZ296526 AZ296526.1 GI:9538 GSS. Mus musculus (house Mus musculus	RA

COMMENT JOURNAL MEDLINE PUBMED

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FEATURES
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Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Golobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Dackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J.A., Bradt, D., Bruist, C., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Waglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, R.B., Ramachand, M., Sandellin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R., Shimada, K., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY708009 RIKEN full-length enriched, adult male s musculus cDNA clone 2010001M19 5', mRNA sequence.
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Class: BAC ends.
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/clone="RPCI-23-160G18"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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URL:http://genome.gsc.riken.go.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Hori,F., Imotani,K.,
S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K.,
Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno
H., Koya,S., Miyazaki,A., Murata,M., Nakamura,N., Nomura,K.,
Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H.,
Sasakki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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The Institute of Physical and Chemical Research (RIKEN)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDMAs
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Tel: 81-45-503-9222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/note="Site 1: XhoI; Site 2: SstI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                   contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue type="small intestine"
/dev_stage="adult"
/lab_host="SOLR"
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(mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sex="male"
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          Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Alzawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Watsuda, H., Ashburner, M., Batalov, S., Casavant, T., Kadota, K., Watsuda, H., Ashburner, M., Batalov, S., Casavant, T., Kuchl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Kochiwa, H., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gatiboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N.H., Lyons, P., Nordone, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Sato, K., Schombach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Wilhita, Y., Kothenki, S.
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Mus musculus adult male small intestine enriched library, clone:2010001M19 produ (Drosophila), full insert sequence.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Hasegawa, Y.,
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Analysis of the mouse transcriptome of 60,770 full-length CDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted (10-JUL-2000) Yoshihide Hayashizaki The Institute Physical and Chemical Research (RIEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GRIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0 and subtraction to Rot = 20.0. Second strand cDNA was prepared with the primer adapter
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6 (bases 1 to 1540)
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21085660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prepare mouse tissues. First strand cDNA was primed with a primer
[5' GAGAGAGAGAGACCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11217851
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/proteIn_id="BAB25411.1"
/db_xref="GI:12841942"
/db_xref="MGI:12841942"
/db_xref="MGI:893591"
/translation="MAPHPLDALTIQVSPETQQPFPGASDHEVLSSNSTPPSHTLIPR
/translation="MAPHPLDALTIQVSPETQQPFPGASDHEVLSSNSTPPSHTLIPR
DCSBABVGDCRGTSRKLRARRGGRNRPKSELALSKKRRSRRKKANDRERNRMHNLNSA
LDALRGVLPTFPDDAKLTKVETLRFAHNYIWALTQTLRIADHSLYGPEPPVPCGELGS
                                                                                                                                                                                                                                                  BLASTN,
                                                                                                                                                                                                                                                                            note="unnamed protein product; atonal homolog 5 (Drosophila) (MGD|MGI:893591, GB|NM_009719, evidence:
                                                                                                                                                                                                                                                                                                                                                        /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="FANTOM_DB:2010001M19"
/db_xref="MGI:1907403"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                        Drosophila)
                                                                                                                                                                                                                                                                                                                                                                                              tissue_type="small intestine"
clone_lib="RIKEN full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="2010001M19"
                                                                                                                                                                                     codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for Genome
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PGGGSNGDWGSIYSPVSQAGNLSPTASLEEFPGLQVPSSPSYLLPGALVFSDFL"

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RESULT 5
BX524720
ID BX52
XX BX52
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TITLE
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BX445903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2626.r
Contact: Feng Liang Email: filang@lifetech.com VRL:
http://fulllength.invitrogen.com/ Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID: CS2BAX8ZA08_AX14ZE4_1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 923)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BX445903 Homo sapiens FETAL BRAIN Homo CSODF015YD06 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                    standard;
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 (Rel.
                                                                                                                                                                                                                               Conservative (
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larity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                  /note=Torgan: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECORV sites of the pCMVSPORT 6 vector. Library was not normalized."

290 c 214 g 251 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                         tissue_type="FETAL BRAIN"
dev_stage="fetal"
                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="CSODF015YD06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            mol_type="mRNA"
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AUTHORS
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ORGANISM
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Best Local Similarity
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Korn B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further inform Seq primer: T7, Primer sequence: TAATACGACTCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Mouse UnigeneSet - RZPD2 (RZPDLIB No.981)
http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RZPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
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Tel: +49 30 32639 101
Fax: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RZPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (28-MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          www.rzpd.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Ina Rolfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RZPD; IMAGp9980187204.
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1 (bases 1 to 517)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                              BU053975 517 bp mRNA
UI-M-FDO-bzg-h-11-0-UI.rl NIH_BMAP_FDO Mus
IMAGE:6403258 5', mRNA sequence.
                                                                                                                                                                                                                                                                           23;
                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                Mus musculus
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                                                                                                                   BU053975
                                                                              Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                              BP;
                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Cloned unidirectionally. Primer: Oligo dT. Size-eelected 1.5 kb for average insert size 2 kb. Pr library; non-amplified. This library was constructed Mione (University College London, Dept of Anatomy and Developmental Biology)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                             90 A; 162 C; 192 G;
                                                                                                                                                                                                                                                                                                                                                       /dev_stage="13.5 dpc"
/lab_host="DH12S"
                                                                                                                                                                                                                                                                                                                                                                               clone="IMAGp9980187204"
clone_lib="Mione mouse WTB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/note="Cloned unidirec
                                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
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                                                                                                        GI:22494052
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Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                      1.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Berlin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   od.de) for further information. sequence: TAATACGACTCACTATAGGG
                                        Chordata;
Rodentia;
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Pred. No.
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                                        Craniata; Vertebrata;
Sciurognathi; Muridae;
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Contact: Klein WH
Department of Biochemistry and Molecular Biology
                                                                                                                    Mu,X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W., White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H. Gene expression in the developing mouse retina by EST sequencing and microarray analysis
                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is TGAGACAGCC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Instututes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
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/lab_host="PH10B (T1 phage resistant)"
/clone lib="NIH BMAP FD0"
/clone lib="NIH BMAP FD0"
/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNa was size fractionated on a 1% agarose
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strain="C57BL/6"
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23; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Texas M.D. Anderson Cancer Center Box 117, 1515 Holcombe Blvd., Houston, TX 77030, Tel: 713 792 3646
                                                                                                                                                                                                                                                                                                                                Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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National Institutes of Health, M
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Mammalia; Eutheria;
1 (bases 1 to 673)
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http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122
                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE: 6808442"
/tlosue_type="whole brain"
/tlosue_type="whole brain"
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/clone_lib="NIH_BMAP_FR0"
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/clone_lib="NIH_BMAP_FR0"
/clone_lib="NIH_BMAP_FR0"
/clone="Organ: Brain; Vector: pyx- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pyx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Institute of Mental Health (NIMH), Hemin Chin, program coordinator."
219 c 250 g 81 t 1 others
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/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
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                                                                    GI:27433882
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Pred. No.
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REFERENCE
AUTHORS
TITLE
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SOURCE
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BU058877
LOCUS
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VERSION
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                                                                                                                                             REFERENCE
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                                                                      TITLE
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                                                                                                               AUTHORS
                                        JOURNAL
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National Ins
Unpublished
Contact: Rob
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                                                                                                                                                                                                                                                                                                                                                                                                                                    BU058877
UI-M-FRO-cak-k-23-0-UI.rl NIH_BMAP_FRO Mus
IMAGE:6413710 5', mRNA sequence.
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23; Conser
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Email: Gapbs-remail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muri
1 (bases 1 to 687)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 689)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                 BU058877.1 GI:22499166
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//dev stage="mbhyo 12.5 dpc"
//lab_host="DH10B (TI phage resistant)"
//clone lib="NIH BMAP FD0"
//clone lib="NIH BMAP FD0"
//clone lib="NIH BMAP FD0"
//clone lib="NIH BMAP FD0"
//note="Organ: brain; Vector: pXX-Asc; Site_1: EcoR I;
//note="Organ: brain; Vector: pXX-Asc; Vector: The library tag
//note="Organ: brain; Vector: The library tag
//note="Organ: brain; Vector: pXX-Asc; Vector: The
//note="Organ: brain; Vector: pXX-Asc; Vector: pXX-Asc; Vector: The
//note="Organ: brain; Vector: pXX-Asc; Vector: 
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228 c 250 g 91 t 1 others
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100.0%; Pr.
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Pred. No.
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Sciurognathi;
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thi; Muridae; Murinae; Mus
                                                                          Gene Collection (MGC)
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Robert Strausberg, Ph.D

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REFERENCE
AUTHORS
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       732 GAGCGCAACCGCATGCACAACCT 754
                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UI-M-FR0-cbc-k-21-0-UI.r1 NIH BM
UI-M-FR0-cbc-k-21-0-UI 5', mRNA
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                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                  Unpublished
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/lab_host="DH108 (T1 phage resistant)"
/clone lib="NIH BMAP RR0"
/clone lib="NIH BMAP RR0"
/clone lib="NIH BMAP RR0"
/note="Organ: Brain; Vector: pYX- Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
M. Bento Soares, bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           program coordinator."
228 c 255 g
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clone="IMAGE:6413710"
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; Pred. No. 5;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 814)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQ178789 814 bp mRNA linear UI-M-EVO-bwt-k-07-0-UI.rl NIH_BMAP_EVO Mus musculus
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
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                                                                                                                                                           This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                     primer: pYX-5
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//dev stage="embryo 13.5,14.5,16.5,17.5dpc"
//lab_host="DH10B (TI phage resistant)"
/clone lib="NIH BMAP FRO"
/clone lib="NIH BMAP FRO"
/clone lib="NIH BMAP FRO"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lemnon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with Oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
264 G 264
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/mol_type="mRNA"
                           organism="Mus musculus"
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clone="UI-M-FR0-cbc-k-21-0-UI"
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Pred. No.
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'strain="C57BL/6" 'db_xref="taxon:10090" 'clone="IMAGE:5701758"

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RESULT 14
BU054481
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Best Local
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23; Conser
                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 823)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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UI-M-FDO-bzj-i-24-0-UI.rl NIH_B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMAGE:6404447 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                    Seq primer: pYX-5
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/dev_stage="embryo 15.5 dpc"
/lab_host="PH10B (TI phage resistant)"
/clone_lib="NIH_BMAP_EVO"
/clone_lib="NIH_BMAP_EVO"
/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according to
Sonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNa was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pYX-Asc vector. The library tag
sequence_located between the Not I site and the polyA tail
, is GTGCGTGGAA. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Instututes of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."

2018
/dev_stage="embryo 12.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_FD0"
                                                                              tissue_type="whole brain"
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                                                                                                                                                                /strain="C57BL/6"
                                                                                                                                                                                         mol_type="mRNA"
                                                                                                                                                                                                                     organism="Mus musculus"
                                                                                                                                                                                                                                                                           ocation/Qualifiers
                                                                                                          one="IMAGE: 6404447"
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; Pred. No. 5.1;
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe and Dr. Mina
CDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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AGENCOURT 11295215 NIH MGC 164 Mus
IMAGE: 30146192 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plate: NDAM0061 row: h column: High quality sequence start: 16 High quality sequence stop: 640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CA979119.1 GI:27511773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 932)
      153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according to BonaTdo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarcse gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is TGAGAGAGCC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Instututes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
ค
                                                                                      /clone="IMAGE:30146192"
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/clone lib="NIH MGC 164"
/note="Vector: pCMV-SpORT6.1.ccdb; Site_1: EcoRV; Site_2: /note="Vector: pCMV-SpORT6.1.ccdb; Site_1: EcoRV; Site_2: /note="Vector: pCMV-SpORT6.1.ccdb; Site_1: EcoRV; Site_2: /note="Not1; Non-normalized full-length enriched library from pooled mouse embryonic limb, maxilla and mandible, day 10.5 and 11.5 (size selected for the 0.5-1 kb fragments) 11.5 (size selected for the 0.5-1 kb fragments) Cloned directionally, priming method: 011go-dT cDNA enrichment: >1k bp, Average insert size 1.8k bp. Priming sequence: 5'GACTAGTTCTAGATCGCGAGCGGCCCC(T) 3'. Tissue
contributed by, David Rowe. Library constructed by ResGen
Invitrogen Corp."
349 c 276 g 153 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.6%; Score 23;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13; Length 823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA linear EST 06-JAN-2003 musculus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 5.2;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 732 GAGGGCAACCGCATGCACAACCT 754

Db 561 GAGCGCAACCGCATGCACAACCT 583

Search completed: January 29, 2004, 22:18:31

Job time: 2908 secs

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